



Sequence Listing

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Botstein, David
Desnoyers, Luc
Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljasin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Val Thr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	440	445	450
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
ctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagctttctg gtgscntttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataacct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
agaataacc ccagcaaca actggtgagc acgagcaaca cagtcacggc 300
gccccacatc aagaagttca ccttcgtctg catggctctg tcactcagc 350
ttgttttctg gatgttttgg acaccccaag tgcctgngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gggatcttcc tctttcttcc cagttccagt cacagtgagg ggcacatcca 500
ccgggtggtt gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 272,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tggagctatc caggatcgc tttcttgtt tggagagat ccccccagac 50
ccttccttg ggtttttttt ccccccagtc ccccccagac ccccccagac 100
agttcagcctt ngtttgnata gntctgtcaa ctccagctnt atttctaat 150
gttttggaca ccccaagtat ttgaqaaaat tttgataqac atnatcggag 200
tggantttgc ctttgcagaa ntttgnngntg ttcttttgcg gattttctcc 250
tttttccag ttccagtcac agnqagtttt catctcagct ggngantgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400
gcgacctggg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50
acactgaaga aaaccttngt ccttgccccc agntttgtgn tgcggatnat 100
cgtcctcctc gccagcctng tggtcctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
tctatctcttc cctctccc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tctatctcttc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gactgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
ctaggagaca ggccttgacc cggggatcg agatgtaca ggagg 47

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
cctcccgagcc cggcgccggg cgcctgaagg cgggaaccac cgcctatggg 50
gactgactgg gagcctgtct cctgtccagc tgcgcgtcct gcctctggg 100
ctctgacacc tgcctatgtg ggcctgtgtg ccccgccacc cgcgaactca 150

cogtgagcgc cctcatcttc acgttcttcc tcttctggg ggtgctggtg 200
tccatcatta tgcagagccc gggcgtggaq agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcttg cagggccaca 300
tcgactgtgg ctccctgctt ggcacccgcg ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttt accctgctca tgctctgctt 400
gagcagcage cgggaccccc gggtgccat ccagaatggg ttttggttct 450
ttaagtctct gatcctggtg ggctccacg tgggtgcctt ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttggcgctcg tgggtcctt 550
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tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tgaactaac tgagcccage ggtgccacg 750
agggcaaggt ctcatccage ctcaacctca cctctctct ctacgtctcc 800
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ccctatccag tatcctgaa cagaaatgca accccattt gccaacccag 950
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gatgatcage acgtggacgc ccgtgtgggt gaagatctgt gcagctggg 1350
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aacgcgcact tcagctgagg cagcctcaca gctgcacac tggtgccctc 1450
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
caccaatcag ccagctgag ccccaacccc tgcccagct ccaggacctg 1550
ccctgagcc gggccttcta gtgtagtgc cttcagggtc ccaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650
 cctcttcctt cccctctccc ctgttgccca tactcagcat ctcgatgaa 1700
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga cctgcccccc ttctggact tegtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1 5 10 15
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65 70 75
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80 85 90
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95 100 105
 Ala Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110 115 120
 Ser Ser Arg Asn Ile Phe Thr Val Ser Val Ser Tyr Phe Ile Phe
 125 130 135
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140 145 150
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155 160 165
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu
185 190 195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr
200 205 210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
215 220 225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe
230 235 240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala
245 250 255

Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu
260 265 270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser
275 280 285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro
290 295 300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr
305 310 315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile
320 325 330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His
335 340 345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met
350 355 360

Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu
365 370 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr
380 385 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met
395 400 405

Met Tyr Thr Thr Asn Thr Tyr Arg Thr Glu Thr Thr Ala Tyr Met
410 415 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp
425 430 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu
440 445 450

Leu Arg Asn Arg Asp Phe Ser
455

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcattccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
ctttctccac ttctgcttg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cttgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc accg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtccct gagcgctcaa gtttgctcgt 150
aggctcgagag aaggccatgg aggtgccgcg accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttcccccag tctttgctgc cgaagctgtg 250
actgcgcgatt cggaaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggacottgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccgglttgat gctgtgcaat ctgcacatcg tctgccaca 550
cgaggcttca ttcttatgg ctggcgtgg ggttgagaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacaactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750
agccttgctg ggcactcctg taggaggcct gctgatggca ttccagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
atgctaagaa aattgaagca ctgctaaacc ttctagaaa cccttcagta 1000
atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050
gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100
tctttggtca gctgtctgac aaatttaagt gctggtagct gtggtggcag 1150
tggtttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200
gtactctcac ttacttata cttaaattta aatacatact tatgtttgta 1250
ttaatctata aatatatgca tacatggata tatccacca cctagatttt 1300
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
t. 1351

<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

<400> 28
Met Glu Val Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
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Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30
Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
35 40 45
Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
50 55 60
Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
65 70 75
Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
80 85 90
Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
95 100 105
Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
110 115 120
Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 24

cggaagtcgc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggacottgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

atggtttacc aacaaacatc ttgagtggtg ttgggttacc ttatattacc 250

tgggtttgat gctgttgatc ctgcacatcc tctgtgacac cggagcttcc 300

ttcgtttatg gctggcgcgc aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

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ccacccacgt ctgcgttgcg gcccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtccaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgct 250
gctaattgga attgctgcgt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcattctctt gttcctgatt 350
gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttctatt tattgttcag tttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500
gttggttggg acaatacggc aagtgcctga aatgacatcc agagaaatct 550
aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgtctggcta 600
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gaatatgctg gagaggtttt gagatttgtt ggtggcattg gctgttctt 700
cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
agaaaagacc cccgcgcgaat cctagtgcct tcttttgatg agaaaacaag 800
gaagatttcc ttctgtatta tgatcttgtt caatttctgt aattttctgt 850
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ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
cctttcttag catttttacc tgcagaaaaa ctttctatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactgggtat aattatatgt 1150
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tctgttatg ttaagggaaa tccaaattcc 1250
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaaatg ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaacia gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattgtt aaataccgtt ttcatgaaat 1650
 ttctcagtat tqtaacagca acttgtcaaa cctaagcata tttqaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tqtgtggctc tglatatctt 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30
 Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
 35 40 45
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
 50 55 60
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
 65 70 75
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
 80 85 90
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Gln Gln Gln Gly
 95 100 105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37
 <211> 390
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336
 <223> unknown base

<400> 37
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 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100
 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200
 gttcogaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250
 tgacacactn gtgctcgcaa tgtgctccaa tcataggaga atatgctgga 300
 tgggttggc gttgtgtgg gttgtgtgg gttgtgtgg gttgtgtgg 350
 tttctggat attagggtga attagggtga attagggtga attagggtga 400

<210> 38
 <211> 566
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 27

<223> unknown base

<400> 38

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ttacaccaat gtattctaga atagttatgt cttaggaaat tgtggtttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgog 350
ttggcccacg tagcaaaaaq atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcataattga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgtctqaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 560

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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tttttttagc ccttgaacc aggagcaaca gggncagct ccttggaggt 100
tgattggcaa caatcacggc caagtgactc cgcaaataac atcccagaga 150
aatcttaaac tgtgtgggtt tccgaagtgt taacttaaat gacactgtc 200
tggatngctg tgttaaaagt gaccaactgt gctggccatg tgcaccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence
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```
<400> 41
gagaatatgc tggagagg 18
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<220>
<223> Synthetic oligonucleotide probe

```
<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence
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```
<400> 43
ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45
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```
<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens
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gtagctggag tgtgagggag ctgtctgaga ttggggagag agctggcaca 150
tggaggatga cttgactgat gcaaggggag ctggcttctc ggtaaggcc 200
cacactttca gtgaacctt ccacctgatt gtgtcttatg actggctgat 250
ctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gttgccagga ctggcaagac tggccaactga ctccaggtgac cttctaccga 350
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gatggctcag ctctgggtcc ccccgggcct aacagggaaat tctccatcac 400
cgtgggtacaa aaggcagaca gggggcacta ccactgcagt ggcctcttcc 450
agagccctgg tcttgggac ccagaaacag catctgttgt ggctatcaca 500
gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550
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ctcctctgt atccagat gggcttctt ctcaaacaca tccaggatct 1000
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cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200
tttgtagaa taatgtagt aggtgagtg aaataaatt atataaagt 1250
agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
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ggggcaattt tgcnnccag aggcatttg gcaatgttg gagacatttt 1450
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ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgccaaac accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45

<211> 359

<212> PRT

<213> Homo sapiens

<400> 45

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Leu	Gly	Val	Leu	Trp	Val	Ala	Gln	Met	Leu	Leu	Ala	Ala	Ser	Phe	20	25	30	
Glu	Thr	Leu	Gln	Cys	Glu	Gly	Pro	Val	Cys	Thr	Glu	Glu	Ser	Ser	35	40	45	
Cys	His	Thr	Glu	Asp	Asp	Leu	Thr	Asp	Ala	Arg	Glu	Ala	Gly	Phe	50	55	60	
Gln	Val	Lys	Ala	Tyr	Thr	Phe	Ser	Glu	Pro	Phe	His	Leu	Ile	Val	65	70	75	
Ser	Tyr	Asp	Trp	Leu	Ile	Leu	Gln	Gly	Pro	Ala	Lys	Pro	Val	Phe	80	85	90	
Glu	Gly	Asp	Leu	Leu	Val	Leu	Arg	Cys	Gln	Ala	Trp	Gln	Asp	Trp	95	100	105	
Pro	Leu	Thr	Gln	Val	Thr	Phe	Tyr	Arg	Asp	Gly	Ser	Ala	Leu	Gly	110	115	120	
Pro	Pro	Gly	Pro	Asn	Arg	Glu	Phe	Ser	Ile	Thr	Val	Val	Gln	Lys	125	130	135	
Ala	Asp	Ser	Gly	His	Tyr	His	Cys	Ser	Gly	Ile	Phe	Gln	Ser	Pro	140	145	150	
Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	155	160	165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	170	175	180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	185	190	195	

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Sin	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tggtctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggaac tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
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ccacccagaag tttagacctc tttagtagca ggaggctgga agaaaggaca 100
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ccacctaaac gtggacacct atggccgttc cactctgaaa gtgcccagaa 200
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tctaaatacc agaggggaaga tgcccatagc actaggactt ggtcatcatg 1950
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 tgggtctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Tyr Ile Thr Tyr Tyr Lys
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
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<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 tatcgaagaa atcccaacaa g 24

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaaq tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

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ctaactctac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000
aatttctgac aaaggtattg gaagagcttt ccactctcat gatgttatga 2050
ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

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Pro Lys Ser Arg	Ile Asp Tyr Asn His	Pro Gly Arg Val	Leu Leu
	185	190	195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr	Ala
	200	205	210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr	Val
	215	220	225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr	Gly
	230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu	Leu
	245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg	Pro
	260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu	Val
	275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser	Gly
	290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser	Gln
	305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala	Thr
	320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu	Pro
	335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr	Pro
	350	355	360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val	
	365	370	

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

ccagtgcaca gcaggcaacg aagc 24

<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

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<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	215	220	225	
Gly	Thr	Ala	Ile	Ile	Phe	Arg	Phe	Gly	His	Met	Gly	Thr	Gln	Gln	230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Ser Met Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val	
				575					580					585	
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe	
				590					595					600	
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile	
				605					610					615	
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu	
				620					625					630	
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp	
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Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu						
				650					655						

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

gacgcacatc ctcagtcctc gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

agatgatag cgggtacat tctctgatt ggattactta ggaacacac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<211> 453

<212> 187

<213> Homo sapiens

<400> 69

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20 25 30

Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro
35 40 45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

	50		55		60
Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly	65		70		75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala	80		85		90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	95		100		105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe	110		115		120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly	125		130		135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr	140		145		150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe	155		160		165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys	170		175		180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala	185		190		195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg	200		205		210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu	215		220		225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His	230		235		240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala	245		250		255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile	260		265		270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His	275		280		285
Leu Val Gly Tyr Ile Val Tyr His Gln Tyr Tyr Tyr Pro Tyr Arg	290		295		300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr	305		310		315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu	320		325		330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala					

	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val	Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser	Phe
	410	415	420
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr	Arg
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 <223> Synthetic oligonucleotide probe

<400> 71
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<210> 72
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<400> 72

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<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
				20					25					30
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
				35					40					45
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Ile	Val	Lys	Ser	Phe	Asp
				50					55					60
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
				65					70					75
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80					85					90
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
				95					100					105
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
				110					115					120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

ttccaaggct tcttgatgg cagatgattt tgggggtttg cattgtttcc 50

ctgacaacga aaacaaaaca gttttgggaa ttccaggagg gaantccagc 100

ctaccaggga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200

gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcaatgagc ctccacagca gtgggggaga 300

aggaagggtt gggcccagt tccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntgggtgcaa nttaatgctn tgatatggt 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgtttctgg ctcaggg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 78
tacctgcacg atgggcac 18

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
caatgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
tactatgctga actcttcagg ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 83
gtgcaaccaa cagatacaaa ctcttccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
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atgatctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
aacacacccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250
ctggatacaa aagtacaatc tttactgtgt aaatacatgt atatgtacta 300
tatgaaaata taccaaatat caataatact tatctctggg taaaaacctc 350
ttctcatacc ctgtgctaac aacttttaac aaaaaatttg catcactttt 400
aagaatcaag aaaaatttct gaaggtcata tgggacagaa aaaaaaacca 450
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 20 25 30
 Thr Ser Met Pro Gln Ala Thr Ala Ala Gln Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaagggca agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

<400> 89
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aggcgggcgc gccacaccca gacgggcccc ccgcggcaga cggcgaaggac 200
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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20					25				30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40					45

Ala Asp Gly Pro	Pro Ala Ala Asp Gly	Glu Asp Gly Gln Asp	Pro
50		55	60
His Ser Lys His	Leu Tyr Thr Ala Asp	Met Phe Thr His Gly	Ile
65		70	75
Gln Ser Ala Ala	His Phe Val Met Phe	Phe Ala Pro Trp Cys	Gly
80		85	90
His Cys Gln Arg	Leu Gln Pro Thr Trp	Asn Asp Leu Gly Asp	Lys
95		100	105
Tyr Asn Ser Met	Glu Asp Ala Lys Val	Tyr Val Ala Lys Val	Asp
110		115	120
Cys Thr Ala His	Ser Asp Val Cys Ser	Ala Gln Gly Val Arg	Gly
125		130	135
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro	Gly Gln Glu Ala Val	Lys
140		145	150
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr	Leu Glu Asn Trp Met	Leu
155		160	165
Gln Thr Leu Asn	Glu Glu Pro Val Thr	Pro Glu Pro Glu Val	Glu
170		175	180
Pro Pro Ser Ala	Pro Glu Leu Lys Gln	Gly Leu Tyr Glu Leu	Ser
185		190	195
Ala Ser Asn Phe	Glu Leu His Val Ala	Gln Gly Asp His Phe	Ile
200		205	210
Lys Phe Phe Ala	Pro Trp Cys Gly His	Cys Lys Ala Leu Ala	Pro
215		220	225
Thr Trp Glu Gln	Leu Ala Leu Gly Leu	Glu His Ser Glu Thr	Val
230		235	240
Lys Ile Gly Lys	Val Asp Cys Thr Gln	His Tyr Glu Leu Cys	Ser
245		250	255
Gly Asn Gln Val	Arg Gly Tyr Pro Thr	Leu Leu Trp Phe Arg	Asp
260		265	270
Gly Lys Lys Val	Asp Gln Tyr Lys Gly	Lys Arg Asp Leu Glu	Ser
275		280	285
Leu Arg Glu Tyr	Val Glu Ser Gln Leu	Gln Arg Thr Glu Thr	Gly
290		295	300
Ala Thr Glu Thr	Val Thr Pro Ser Glu	Ala Pro Val Leu Ala	Ala
305		310	315
Glu Pro Glu Ala	Asp Lys Gly Thr Val	Leu Ala Leu Thr Glu	Asn
320		325	330

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
				335					340					345	
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
				410					415					420	
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
				425					430						

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91

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<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

atgagcacc acactctaca a 21

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 93

aagtggctgc cttgtgcaac gtgc 24

<210> 94

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
ggtc aaaggg gatata tgcg cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gc atg gaaga tgcc aaagtc tatgt ggcta aagtgg actg cacgg ccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200
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ggtc atgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800

agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850
 agtaacttcc ctcatcctac gtatttgcta ttttcctgtg accgtcatta 900
 cagttattgt tatccatcct ttttttcctg attgtactac atttgatctg 950
 agtcaacata gctagaaaaat gctaaactga ggtatggagc ctccatcatc 1000
 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
 Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu
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 Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile
 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200		205		210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn					
	215		220		225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser					
	230		235		240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly					
	245		250		255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys					
	260		265		270
Glu Phe Ile Lys Lys Lys Lys					
	275				

<210> 98
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
 cgctgactat gttgccaaga gtgg 24

<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
 gtgttcattg gcgtgaatga ccttgaagg gaggacact acatgttcac 50

<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250
gtcccatggc tgcctcctg ctgtgcccc tctgtctgtt gctaccgtg 300
ctgtctctga agctacacct ctggccgcag ttgcgtggc ttccggcgga 350
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cagcacagg tgacgtgtt ccagtacatt ggggagctgt gccgatact 1400
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 gccctagatt ttcttcagga ggtgaacgtc tatggagtca ctgtgccagg 2000
 gcctgaaggg agggctggaa tggcagccct agttctgctt ccccccaag 2050
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 gaccttcaaa cagcagaaaag ttgggatggc aaatgagggc ttgcaccca 2200
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 cgggcaca cctctctc gaa 2574

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp
500		505	510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys	Met
515		520	525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val	Ser
530		535	540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu	Ala
545		550	555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val	Phe
560		565	570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe	Leu
575		580	585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly	Glu
590		595	600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

<210> 103
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 103
 gagagccatg gggctccacc tg 22

<210> 104
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 104
 jgaagaagtg ggcagaa 18

<210> 105
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
caggtgacag gataactata ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

<400> 108
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100
aaggcgccat acacactcgc tctcgcttgt ccatctccct cccgggggag 150
ccggcgcgcg ctcccacctt tgccgcacac tccggcgago cgagcccgca 200
ggcctccagg attctggggc tcggaactcg gattgcagct ctgaaccccc 250
atgggggttt tttaaacact tcttttccct ctcttctcg ttctcattga 300
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acgttgggca gggcgagga gggcgagct gctcttggcg ggctttcgga 500
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 gtgagggttt tttttttctc atttaaaat 2579

<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Ile	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
				545					550					555

<210> 110

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

aagcgtgaca gcgggcacgt c 21

<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

cgcacagtct ctgcagtggc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

<400> 113
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aataagttag ctgagaaaac gcacgcagtt tgcagcgctt gcgcgggtg 100
cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200
tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250
tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300
aaaggactgg ggaaaatagc cctgggaaaag tggagaaggt gatcaggagg 350
ccggctccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400
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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114

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Gln	Ala	Cys	Val	Cys	Pro	Gly	Lys	Met	Leu	Ala	Met	Gly	Ala	Leu	20	25	30	
Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

cccaacccaa ctgtttacct ctgg 24

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

gccacactac ctacagaaact gaaggaggtt gqntatitcaa cgcatatggt 50

cgq 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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1				5					10					15

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	230	235	240
Gly	Ser	Phe	Lys	Lys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gagagctgct gctgtggctg ctgggtgctgt gccactact cctgctcttg 50

gtgcagctgc tgcgcttact gagggctgac ggcgaactga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatgggtg 150

tgtgqatgac tgaagcctcg agtggaaatg gtgaggagct ggcttaccag 200

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 gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25				30	

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40				45	

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55				60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Gln	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285
Thr	Lys	His	Asp														

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

ggtatgaatctatgacacggtg 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatggggc gagtggcagg gacgacgccc agaata 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
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caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgtttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
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<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
1				5					10					15

Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20						25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn		50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln		65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val		80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu		95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu		110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro		125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu		140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln		155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly		170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu		185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn		200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met		215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly		230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp		245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln		260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp		275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro		290	295	300
Glu Thr Pro Glu Met Ser Asp Gln Asp Ser Cys Val Ala Cys Gly		305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcacc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgcgc ccggccccca ttcgggccgg gcctcgctgc ggccggcgact 50

gagccagggt ggcccgctgc cctgagtcgc agagtccggc cggccgggca 100

ggggcagcct tccaccacgg ggagcccagc tctcagccgc ctcacaggaa 150

gatgctgggt cggcggggga gccctggcat ggggtgtgat gggggggcag 200

ccctggggagc actgagggtc tgcctccagc gaggcctgga ggt tggg 250

cctgaagacc cagtgggtgc actgggtggg accgatgga cctggtgtg 300

ctcctttccc cctgagcctg gcttcagcct ggcacagctc aacctcctct 350

ggcagctgac agataccaaa cagctgggtgc acagctttgc tgaggggcag 400

gaccagggca ggccttatgc caaccgcacg gccctcttcc cggacctgct 450

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agggcagctt cactgtcttc gtgagcctcc gggatttcgg cagcctctgc 550

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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met	Leu	Arg	Arg	Arg	Gly	Ser	Pro	Gly	Met	Gly	Val	His	Val	Gly
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Ala	Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu
			20						25					30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35						40					45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50						55					60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65						70					75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80						85					90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95						100					105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110						115					120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125						130					135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140						145					150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155						160					165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Gln	Val	Ile	Ile	Thr	Arg
			170						175					180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185						190					195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200						205					210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215						220					225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacatcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

tttatctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

gaacacagta taatgacaa 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgcaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tggaagaaga ggggtgtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 145

gagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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gaaggaggag ttttgaatt gtctgaagaa ttgtttgtg agcttctaat 100

tactttctta aatctatgaa gtctgaggaa atttggctga ttgtgtggg 150

actttcttcc ttgcttcaga aacatgagga tttttttgtg gaagggggtc 200

ttgactctgt tcttcaattc ttgtattggg gctttgatcc ctgaaccaga 250

agtgaataatt gaagtctctc agaaqccatt catctgccat cgcaagacca 300

aaggaggagg ttgtatgttg gtccactatg aaggtactt agaaaaggac 350

ggtctcttat ttacttcac tcacaaacat aacaatggtc agcccatctg 400

gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggcttga 450
aaggaatgtg tgtaggagag aagagaaagc tcacattcc tctgctctg 500
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tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750
aagacaaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
gagttataga gatacatcta ccccttttaat atagcactca tctttcaaga 850
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 gcagctacta ttgaataaat acctatcttg gatttt 2336

<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30

Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35					40						45

Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50					55						60

Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65					70						75

Pro	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80					85						90

Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Ile	Thr	Ile
			95					100						105

Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110					115						120

Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125					130						135

Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140					145						150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 146
 ctttccttgc ttcagcaaca tgaggc 26

<210> 147
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 147
 gccagagca ggaggaatga tgagc 25

<210> 148
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 148
 gtggaacgag gtcttgactc tggctgtcac ttctttgatt ggggctttg 49

<210> 149
 <211> 2196
 <212> DNA
 <213> Homo sapiens

<400> 149
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tttttttagc atccaaccat tcttcccttg tagttctcgc cccctcaaatt 100
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cagagatgcc tggtacctc ggcctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgcca ccaggacgga gcatggaggt cacagtacct 250
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tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
			20						25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Asp	Arg	Leu	Trp	Phe	Ala	Trp	Asn	Leu	Trp	Thr	Val	Asn	Phe	
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<110> 151
 <111> 524
 <112> DNA
 <113> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagttctc tgaaaatgca cagagatgcc tggctacctc 150
 ggcctgcctt cagcctcagc gggctcagtc tctttttctc tttgggtgcca 200
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 ctctc cca agttcctct gcatgcaat tccctctctc ctacacagtc 350
 ctctgaggag atgtttctctc agttcagcag gaagatcatt aaactcaacc 400
 tggagcgggtt tcaagatgag gtggagttct cagggcaacc cagcaagtag 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatcaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacgggggt catctctttt tctctttggt gccaccagg acggagcatg 50
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ccctgaactg gatttaccag gactgcaaca actggctctg aggagatggt 200
ccttcagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcgggtgatg tgagaaacgt gcagccggag gatgagggga ttacaactg 350
ttacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
tcgggtgatg tgagaaacgt gcagccggag gatgagggga 24

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgacct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tggggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50

ggggtgctcc cggatggcct cctgttcttc ttgtgtgtgc taatgtgtgt 100

cggggaccca ggcctccggc cgggacgtca cccccagtg gtgctggctc 150

ctgggtgattt gggtaaccaa ctggaagcca agctggacaa gcgacagtg 200

gtgcactacc tctgtccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgtgtgtgc ctgtcatcat tgactgtgtg attgacaata 300

tcaggctggt ttacaacaaa acatccaggg ccaccagtt tctgatggt 350

gtggatgtac gtgctcctgg ctttggaag acctctcac tggagtctc 400

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tatgaactgg gcgagcccc aatgaaaac gggccctact tctggccct 550

ccgagagatg atcagaggaa tgtaccagct gtatgggggc ccgtggtgc 600

tggttgccc cagtatggg aacatgtaca cgtctactt tctgcagcg 650

cagccgagg cctggaagga caagtatata cgggccttcg tgtcaactgg 700

tgcgcctgg gggggcgtg ccaagacct gcgcgtctg gcttcaggag 750

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cggtcagctg tctccaccag ctggctgtgt cctacaact acacatggtc 850

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actacggcgc gtctcttgg cctatggg ccaacatgc ctgggtcttc 950

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro	
				20				25					30	

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Gln	Gln	Met	Gly	Met	Leu	Tyr	Gly	Ala	Ile	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
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<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
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<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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gaggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
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<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe
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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Ile	Asp	Arg	Ile	Tyr	Leu	Val
				95					100					105

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcgggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaagggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ncacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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ctggggggca gggggaacga ggtgatggcg aggaagagga ggcagaggg 150
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200
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gggtgctact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300
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 <213> Homo sapiens

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Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr	110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly	125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro	140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu	155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val	170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile	185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu	200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg	215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu	230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr	245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly	260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg	275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala	290	295	300
Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val	305	310	315
Leu Ser Val Gln Pro Val Val Ile Ser Ala Tyr Glu Val Asn Leu	320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro	335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His	350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln			

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Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro
	440	445	450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys
	455	460	465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys
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Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile
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Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly
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Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe
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Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro
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Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu
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His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly
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Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu
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Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala	Asp
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Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Ser Val Asp Ser	Met
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Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln
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Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu
	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val
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Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val

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Arg Pro Val Cys Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	
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<212> DNA

<213> Homo sapiens

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<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

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<223> Synthetic oligonucleotide probe

<400> 174

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<223> Synthetic oligonucleotide probe

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<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 178

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Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
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Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
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Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
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Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
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<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

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<400> 181

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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

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gtgtctcccc ttgaggccct agatgggtggc acaggtccag ccgtgaggg 2350
cggggcagtg ggtgggcaag atggggagca ggcaccccca ctgcccacca 2400
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gaagccccag ggccactgcc ctcaactgcc ctgagagccat cactattgtc 2500
tggagtgggt caggccctgc gaggccgtct gttgcacagc ctggggcccc 2550
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gaagatgagg acgatgtgct cctggtcccc ctggtccacc cgggggtgtg 2650
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ttcagggact tcttgggctt ccgttgcac ctatgtagct gctataaaat 2850
taagtgtccc tcaggcaggg agagggtcca cagagtctcc tctgtacgtg 2900

gccatggcca gacaccccag tcccttcacc accacctgct ccccacgcca 2950
 ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
 ggtctggaca ctccatcctt gccaaaacctc taccctaaag tggccttaag 3050
 caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
 ctcacaaaaa gagtgcaca aatgcttcta ttccatagct acggcattgc 3200
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15	
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30	
Pro	Pro	Ala	Val	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45		
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165	
Gly	Asp	Gly	Ser	Asp	Gln	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180	
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr				

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200					205					210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					

470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser		
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp		
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu		
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly		
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg		
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn		
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser		
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg		
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro		
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala		
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro		
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly		
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro		
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp		
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu		
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtocca etc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgctgtctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttggga cagaccctgt ggcttaggt ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgaagctgggc gagaagtagg ggagggcggg gctccgcgcg ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctggggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgccggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcaactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggctcttac 550
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600
 ttttagttt gatactaagt attaaacata ttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 662

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Thr Ile Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Ile
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 212, 234, 487
 <223> unknown base

<400> 191
 gggcgagaag taggggaggg cgtgttcgc cgcggtggcg gttgctatcg 50
 ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
 tctgtgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150
 catcgccctt tctgcttcag tgtgaaaggg cactgaaga tgctgagggt 200
 ggcactaact gngacatcta tgacctttt tatnategca caagcccttg 250
 aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
 atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
 gacttttgctt gatattatca actcactggg aacaacagta ttcattgtca 400
 tcttatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
 ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 192
 cgttttgcag aacctactca ggcag 25

<210> 193
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgtc tgctgggtct gcagacgca tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgcgggccga gtcgtgagc cgcggctgcc ggacgggacg 50
ggatgggcta ggctgggcgc gcccccggg ccccggcgtg ggcattggcg 100
caatggcccc ggctgtgtc ctgctctgc tggcccagt gctcctgcgc 150
ggcgccccgc agctggcccc cgcgccttc acgtgcccc tcgggtggc 200
cgcgccacg aaccgcgtag ttgcgccac ccggggacc gggacccctg 250
ccgagcgcca cgcgcacggc ttggcgctcg cctggagcc tgcctggcg 300
ccccccgcgg gcgcgcgcaa cttcttggcc atggtagaca acctgcaggg 350
ggactctggc cgcggctact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450
ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500
cagataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550
actggacggg ctctgttggg gaagacctcg tcacatccc caaaqgcttc 600
aatacttctt ttcttgcgaa cattgcacat atttttgact cagagaa 650
ctttttgcct gggattaaat ggaatggaat acctggccta gcttatgcca 700
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acacaagcaa acatccgcaa cgtttttctc atgcagatgt gtggagccgg 800
cttccccgtt actggatctg ggaaccaagg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagana tctggtatac cctattaag 900
gaagagtggc actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaal ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
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ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttgg 1150
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caccgtctt caatctctgt tctgtccca gatgccttct agattcactg 1800
tcttttgatt ctgattttc aagctttcaa atctcccta ctccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln
1 5 10 15

Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
20 25 30

Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
35 40 45

Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
50 55 60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala			
				65					70					75			
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg			
				80					85					90			
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu			
				95					100					105			
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly			
				110					115					120			
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser			
				125					130					135			
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr			
				140					145					150			
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile			
				155					160					165			
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile			
				170					175					180			
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly			
				185					190					195			
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser			
				200					205					210			
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro			
				215					220					225			
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala			
				230					235					240			
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu			
				245					250					255			
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu			
				260					265					270			
Gln	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly			
				275					280					285			
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Gln	Thr	Asn	Ala	Asp	Lys	Ala			
				290					295					300			
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val			
				305					310					315			
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro			
				320					325					330			
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp			
				335					340					345			

Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
350		355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
365		370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
380		385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu
395		400	405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp
410		415	420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu
425		430	435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr
440		445	450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu
455		460	465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly
470		475	480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg
485		490	495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser
500		505	510
Ser Leu Val Arg	His Arg Trp Lys		
515			

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 197

ggagaagat accgattct 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 198

ggaaaattgga ggccaaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gacttgacct gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggctctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gaagagctta ctctctcttc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgacacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

<400> 205
cgccctccgc ttcggaggct gacgcgcccg ggccgcgttc caggcctgtg 50
cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100
ggggcgggagc cgggagggcg ggccggcatg gaggcgctgc tgcctgggcgc 150
ggggctgctg ctgggcgctt acgtgcttgc ctactacaac ctggtgaagg 200
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 cgctagggt ctcacagtga gtaggaggag ggctgggat ctgaacccaa 1750
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 cagggcaggg cagctggtat cgaggtgccc catgggagta aggggacgcc 1850
 ttccggggcg atgcagggtt ggggtcatct gtatctgaag cccctcgaa 1900
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met Glu Ala Ile Leu Leu Gly Ala Glu Leu Leu Gly Ala Tyr
 1 5 10

Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Lys Gly Gly
 20 25 30

Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
 35 40 45

Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile	80	85	90
Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe	95	100	105
Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile	110	115	120
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe	125	130	135
Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr	140	145	150
His Leu Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val	155	160	165
Val Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe	170	175	180
Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg	185	190	195
Ala Tyr Ala Asp Thr Lys Leu Ala Asn Val Leu Phe Ala Arg Glu	200	205	210
Leu Ala Asn Gln Leu Glu Ala Thr Gly Val Thr Cys Tyr Ala Ala	215	220	225
His Pro Gly Pro Val Asn Ser Glu Leu Phe Leu Arg His Val Pro	230	235	240
Gly Trp Leu Arg Pro Leu Leu Arg Pro Leu Ala Trp Leu Val Leu	245	250	255
Arg Ala Pro Arg Gly Gly Ala Gln Thr Pro Leu Tyr Cys Ala Leu	260	265	270
Gln Glu Gly Ile Glu Pro Leu Ser Gly Arg Tyr Phe Ala Asn Cys	275	280	285
His Val Glu Glu Val Pro Pro Ala Ala Arg Asp Asp Arg Ala Ala	290	295	300
His Arg Leu Trp Glu Ala Ser Lys Arg Leu Ala Gly Leu Gly Ile	305	310	315
Gly Glu Asp Ala Glu Pro Asp Glu Asp Pro Gln Ser Glu Asp Ser	320	325	330
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr	335	340	345
Val Ser Gln Pro Tyr Pro Ser Pro Gln Ser Ser Pro Asp Leu Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
 365 370 375

Leu Ser

<210> 207
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 207
 attcatggcc ttggacttgg ccag 24

<210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 208
 acgcacgtgg cctcaagctg gttg 24

<210> 209
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 209
 attctcagc tetgacccac ggttggacat cctcatccac aatgc 45

<210> 210
 <211> 3716
 <212> DNA
 <213> Homo sapiens

<400> 210
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 caagcctcag gccagccacc tcccaccatc cgtctggttg tgaatgggca 200
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 aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20						25					30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
			35						40					45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
			50						55					60
Leu	Pro	Asp	Gly	Thr	Ile	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
			65						70					75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
			80						85					90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
			95						100					105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
			110						115					120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
			125						130					135

Cys Gly Pro Pro	Trp Gly His Pro Glu	Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln	Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg	Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn	Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln	Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg	Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu	Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser	Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr	Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu	Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg	Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val	Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser	Leu Phe Ile Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu	Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala	Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser	Glu His Gly Pro Trp Thr
425	430 435
Leu Glu Gln Leu Arg Ala Thr Leu Lys	Arg Pro Glu Val Ile Ala
440	445 450
Thr Cys Gly Val Ala Leu Trp Leu Leu	Leu Leu Gly Thr Ala Val
455	460 465
Cys Ile His Arg Arg Arg Arg Ala Arg	Val His Leu Gly Pro Gly
470	475 480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala	Ile Leu Lys His Arg Met
485	490 495
Asp His Ser Asp Ser Gln Trp Leu Ala	Asp Thr Trp Arg Ser Thr
500	505 510
Ser Gly Ser Arg Asp Leu Ser Ser Ser	Ser Ser Leu Ser Ser Arg
515	520 525
Leu Gly Ala Asp Ala Arg Asp Pro Leu	Asp Cys Arg Arg Ser Leu
530	535 540
Leu Ser Trp Asp Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro Asp
545	550 555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser Ser
560	565 570
Thr Pro Ala Arg Pro Ser Pro Gln Val	Pro Ala Val Arg Arg Leu
575	580 585
Pro Pro Gln Leu Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser Asp
590	595 600
Ser Leu Cys Ser Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser Leu
605	610 615
Ala Pro Ala Glu Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu Gln
620	625 630
His Ala Ser Ser Ser Pro Leu Leu Arg	Gly Ser His Ser Leu Glu
635	640 645
Leu Arg Ala Cys Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu Ser
650	655 660
Gln Ser Pro Gly Ala Val Pro Gln Ala	Leu Val Ala Trp Arg Ala
665	670 675
Leu Gly Pro Lys Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr Arg
680	685 690
His Leu Pro Pro Ala Pro Leu Phe Pro	His Glu Thr Pro Pro Thr
695	700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
gaagggaacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
cttcacaggt atccagcacc cagaatgcgg ctctctggtaa tgcctatggg 50
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aggggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150
ctgaggggacc accggaagta ctgggtgcagg aagggtggga tctctttctc 200
tgggtgtctt agcaccatct atgcagaaga agaaggccag gacacaaatga 250
agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

acctgtgga acctaccct gcaagacgt ggggagtact ggtgtgggt 350
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acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500
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<210> 216

<211> 332

<212> FRT

<213> Homo sapiens

<400> 216

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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20				25					30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35				40					45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
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<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
cgtcttctcc ctgcttggt gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
tgtgcaggaa gggtagggatc ctcttctctc gtgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
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cagctggcgc gctctctac tctcctctc ttccccacac taagctgtac 150
cgggtgctac atagctcact acagctcag actcctaac ttgagaaatc 200
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gtatcccaa agctcagctc tgagccaaag tggtagtgc ccacctctc 350
cggcgggat agaagccagg agcagggtc tcagaaggcg gtggtgccca 400

getgggatca tgttgttggc cctggctctgt ctgctcagct gcctgctacc 450
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 atgaattcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
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 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
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 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggtggg aaatgtgggt tggttcctga 900
 cctaggtctg ggaagacaag ccagcgaata aaggatgggt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Met	Tyr	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80										85

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tggtggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggcgggg cgcgcggggc ggcaccatga gtccccgctc 50
gtggttgagt tggctgcgcc tctcctcttt cgcgctcttc tcagccggcg 100
cagcgaactg gctgtaactg gccaaagtgt agtcggggga ggcgaactga 150
gaggaggaga cgtgcgagaa actcaaggga ctgatacaga ggcaggtgca 200
gatgtgcaag ccgaacctgg aagtcatgga ctgggtgggc cgcggtgccc 250
agctggccat tgaggagtgc cagtaaccagt tccggaaccg gcgctgggaa 300
tgctccacac tggactcctt gcccgctctt ggcaagggtg tgacgcaagg 350
gactcgggag gcccgccttc tgaacgcac ctcttcggga ggtgtggcct 400
ttgcagtga cggggcgctg agcagtgagg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaac atcgccacag gtgtggcctt ctcacagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgcg cagggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800
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aattggagcc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900
ctgggcacga gggggccgac atgcaacaag acgtccaagg ccacgcacgg 950
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aaacagtctc ccaccacctc ccccaagaga tactggttgt attttttgtt 1200
ctggttttgt ttttgggtcc tcatgttatt tattgcgaa accaggcagg 1250
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaagggac ctgtctcgtg ccgtggtgt ccgcctgtg 1350
gtgcccactg accactcagt tggttatctgt gtcggttttt ctacttcag 1400
acctaaagtg gagtaacaag gagtattacc accacatggc tactgacct 1450
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ccctgagaaa ggaaacaagg agataccagg tcaagggcac caggttcatt 1650
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gcaagaagag ggagatgaga gcaagagag actgaagtc caccctagaa 1750
cccagcctgc ccagcctgc cctgggaag aaaaaactta accactccc 1800
agaccacct aggcaggcat ataggctgc atcctggacc agggatccc 1850

gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaagg 2000
ctgtgccttt gcagtcatgc cccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe
1				5					10					15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys
				20					25					30
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys
				35					40					45
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn
				50					55					60
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile
				65					70					75
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser
				80					85					90
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly
				95					100					105
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val
				110					115					120
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys
				125					130					135
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe
				140					145					150
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe
				155					160					165
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser
				170					175					180
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg
				185					190					195
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly
				200					205					210
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro

	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Thr Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggtc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

gggacgcgtg ggccggacgc tggggcggac cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggctccacg gagcgcgcgg 250
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300
ggggcgctgg gtgccttgaa ggaagaaatc cgaagctcgc acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcagccgaa gctgatggag caggagagcg cctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggcccgt aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggtccag aacaactcct 550
gcgagccgtg cccacgtcg tggtgtcct tcgagggtc ctgctacttt 600
ttctctgtgc caaagaacgac gtgggcggcg gcgcaggatc actgcgcaga 650
tgccagcgcg caactggtga tcgttggggg cctggatgag cagggttcc 700
tcaactcgaa cagcgtggc cgtgggttact ggctgggctt gagggctgtg 750
cgccatcttg gaaaggttca ccctatcag tgaatggaag gaatctctct 800
tggcttga tctgggacg aggaagacgc caatdaacct tgggggngcg 850
agcaatggtg tctgtgtg caaacgggc tctdaaada cgcacccgtg 900
gacagcgaga aggaaggctg gatctgtgag aaaaagcaca actgctgacc 950
ccgcccagtg ccttggagcc gcgcccatg cagcatgtcc tatcctgggg 1000
gctgtcacc tcctgggtc ctggagctga ttgccaaaga gttttttct 1050
tctcatca cagctgtgca gtctcaaaa ccttgggtc aacataagcc 1100
tgtccagccc agtgcctggg ctctgggacc tccatgcga cctcactcta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200
 ctctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
 1 5 10 15

Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30

Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45

Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60

Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75

Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90

Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135

Glu Ala Gly Arg Gly Arg Ala Asn Val Thr Thr Gln Leu Phe Arg
 140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
 155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
 170 175 180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
 185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
 200 205 210

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgatcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

cacgggtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gacaggggaa gagggtgata cgaacccggg aaqgtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgcgcgcgcgc gcagccctt ctctccttt 100
ctcccacgtc ctatctgoot ctogctggag gccagggcgt gcagcatcga 150
agacaggagg aactggagcc tcattggcgc gcccggggcg ccggcctcgg 200
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggcgc 250
cgctcccgct gctcctgcgc ggtgatggaa aaccccagcc cggccgcgc 300
cctgggcaag gccctctgcg ctctcctcct ggccaactct ggccgcgcgc 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
tacagcatca ccttcacggg caagtggagc cagacggcct tccccagca 450
gtacccctg ttcgcgcgc ctgcgcagtg gtcttcgctg ctgggggcgc 500
cgcatagctc cgaactacgc atgtggagga agaaccagta cgtcagtaac 550
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gatcgaggcg gcgggggagg cgtgcagag cgtgcacgag gtgttttcgg 650
cgccgcgcgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700
cagcgcaggc actcgtcgt ctgctttgtg gtgcgcacgc tgcccagccc 750
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ccgagggcac agggggttcc gcgtcctcc tgaccgcgtt gaggcgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
 aaacagcctc ctctttccc aaccttgctt cttagggggc cccgtgtccc 1500
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 agcggggggc acttgagaag tgaataaatg gggcggttgc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
1				5					10					15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Trp	Gln	Ser	Ala	Gly	Gln	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala
170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	
185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	
200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	
215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	
230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	
245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	
260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	
275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly Arg Leu Gly Phe Lys Ser	
290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	
305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	
320	325	330
Val		

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 237

gaggaagcag agggagagag ag 22

<216> 238

<217> 18

<218> DNA

<219> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 238

caggactcgc taagtcgc 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccccttc tctctcttttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cagccccccttc tctctcttttc tcccacgttc tatctgcttc tc 24

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccccttc tctctcttttc tcccacgttc tatctgcttc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244

ggcggcgctcc gtgagggggt cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggcgg cggccgctc 150
tcaccccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350
ttcatagagt tgtgcttggg ttcatagtc aaggcggaga tctactggc 400
acagggagtg gtggagagtc tatctatgga gcqccattca aagatgaatt 450
tcattcaggg ttgggtttta atgggagagg atggtttccc atggcaaatg 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaaggtta caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
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gaatatattg acggtgctgc aaggtctttt atgagacaaa gaatttccaa 1050
aaaattaaaa aaggacacaa gtggagaatgt taaatcagct ggagaagqaa 1100
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 taacttttct tcacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<110> 245

<111> 472

<112> PRT

<113> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val
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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20					25						30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35					40						45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50					55						60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly
			65					70						75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80					85						90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95					100						105
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
			110					115						120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
			125					130						135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Val Val Gln Lys Thr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser	His	Val	Leu	Gln	Phe	Glu	Asp	Lys	Ser	Arg	Lys	Val	Lys	Asp
				425					430					435
Ala	Ser	Met	Gln	Asp	Ser	Asp	Thr	Phe	Glu	Ile	Tyr	Asp	Pro	Arg
				440					445					450
Asn	Pro	Val	Asn	Lys	Arg	Arg	Arg	Glu	Glu	Ser	Lys	Lys	Leu	Met
				455					460					465
Arg	Glu	Lys	Lys	Glu	Arg	Arg								
				470										

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

caagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

ggcgggagc aggggagc 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactgggaaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
cagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
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tatgtgtccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100
tatttgccct tgttgagggc gtccacccct qcccagacat gtccacaggg 150
ttctccttgg ggtaggggac tctqgactcc atccccggg ccgcccggca 200
gaccagcaca ggccgcgttt tctccttggg aacgggaaag tatagcaacc 250
cttcgtgagg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctcttccaag tggttttgga accgggctct ttggatctaa 350
aactgccact gggttcactc taggaggaac aaatacaggt gccttgcaca 400
ccaagaggcc tcaagtggtc accaaatatg gaacctgca aggaataacag 450
atgcattgtg ggaagacacc catccaactc ttttaggag tccccttctc 500

cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550
cctggaaagg aatcagagat gctaccacct acccgctgg atggagtctc 600
gctctgtcgc caggctggag tgcagtggca cgaatctcggc tcaactgcaac 650
ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700
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gtcagcagc gggaaacggt caagtggctg cgcttcagcg aggactgtct 800
gtacctgaac gtgtacgcgc cggcgcgcgc gcccggggat cccagctgc 850
cagtgatggc ctgggtcccg ggaggcgctt tcacgtggg cgctgcttct 900
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gcctgagggc actatcaggg accaaggtga tgcgtgtgtc caacaagatg 1350
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catgagccct gtggtggatg gtgtggtgat ccagatgac cctttggtgc 1450
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cagcttctg ctgcagcagt acctgacaa tctcaatgag catgactgaa 1600
cgtctctcag acccgtatc atgcacataa ttcaagatgc cactttcgtg 1650
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taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900

cagggcctgg ggagactagc catggacata cctggggaca agagtctac 1950
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 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254

Met	Ser	Thr	Gly	Phe	Ser	Phe	Gly	Ser	Gly	Thr	Leu	Gly	Ser	Thr
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Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe
				20					25					30
Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45
Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60
Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75
Val	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90
Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105
His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
				110					115					120
Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro Glu Pro Trp	Lys Gly Ile Arg Asp	Ala Thr Thr Tyr	Pro Pro
	140	145	150
Gly Trp Ser Leu	Ala Leu Ser Pro Gly	Trp Ser Ala Val	Ala Arg
	155	160	165
Ser Arg Leu Thr	Ala Thr Ser Ala Ser	Arg Val Gln Ala	Ser Leu
	170	175	180
Leu Pro Gln Pro	Leu Ser Val Trp Gly	Tyr Arg Cys Leu	Gln Glu
	185	190	195
Ser Trp Gly Gln	Leu Ala Ser Met Tyr	Val Ser Thr Arg	Glu Arg
	200	205	210
Tyr Lys Trp Leu	Arg Phe Ser Glu Asp	Cys Leu Tyr Leu	Asn Val
	215	220	225
Tyr Ala Pro Ala	Arg Ala Pro Gly Asp	Pro Gln Leu Pro	Val Met
	230	235	240
Val Trp Phe Pro	Gly Gly Ala Phe Ile	Val Gly Ala Ala	Ser Ser
	245	250	255
Tyr Glu Gly Ser	Asp Leu Ala Ala Arg	Glu Lys Val Val	Leu Val
	260	265	270
Phe Leu Gln His	Arg Leu Gly Ile Phe	Gly Phe Leu Ser	Thr Asp
	275	280	285
Asp Ser His Ala	Arg Gly Asn Trp Gly	Leu Leu Asp Gln	Met Ala
	290	295	300
Ala Leu Arg Trp	Val Gln Glu Asn Ile	Ala Ala Phe Gly	Gly Asp
	305	310	315
Pro Gly Asn Val	Thr Leu Phe Gly Gln	Ser Ala Gly Ala	Met Ser
	320	325	330
Ile Ser Gly Leu	Met Met Ser Pro Leu	Ala Ser Gly Leu	Phe His
	335	340	345
Arg Ala Ile Ser	Gln Ser Gly Thr Ala	Leu Phe Arg Leu	Thr Ile
	350	355	360
Thr Ser Asp Pro	Leu Lys Val Ala Lys	Lys Val Ala His	Leu Ala
	365	370	375
Gly Cys Asn His	Asn Ser Thr Gln Ile	Leu Val Asn Cys	Leu Arg
	380	385	390
Ala Leu Ser Gly	Thr Lys Val Met Arg	Val Ser Asn Lys	Met Arg
	395	400	405
Phe Leu Gln Leu	Asn Phe Gln Arg Asp	Pro Glu Glu Ile	Ile Trp
	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgactgc aggagtcttg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacatcagg aagatgaaga tgcg 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtgggtccg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacagggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgcactg ctgtgtcct cgtgtctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcattcttg tgcctgtct tttctctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actgggtcaa agcagtgact gagacaacca 250

aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

accgggggccc gattccagct cactggggat cccgcgaagg ggaactgtct 350

cttgggtgatc agaaacccac aactcccgaa tgagtcacag tacttcttct 400

gggtggagag aggaagctat gtgacatata atttcattgaa cgatgggttc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

caccgacctc acctgccatg tggacttctc cagaaagggg gtgagcgcac 550

agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttggtatc 600

agcatttcac gtgacaacac gccagccctg gagccccaga cccagggaaa 650

tgtcccatac ctggaagccc aaaaaggcca gttcctgccc ctctctgtg 700

ctgtgacag ccagcccccct gccacactga gctgggtcct gcagaacaga 750

gtcctctcct cgtcccctcc ctggggccct agaccctgg ggcctggagct 800

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ctgggttag ctccacacag ccagccctga actctctat ccagtatcct 900

ctg gcttc tggactgct gatttcacaa gcaaacacaa caatcctgga 950

aaactttggg aacggcactt ctctccactt actggagggc caaagcctgt 1000

gcttggcttg tctcacacac agcagcctcc cagccaggtt gacctgacc 1050

cagaggggac aggttctgag cccctcccag cctcagacc cgggggtcct 1100

ccagctgctt cgggttcaag tggagcaca agcagagttc acctgcaacg 1150

ctcggcacc acctgggtcc cagcaggtct ctctcagcct ctccgtgcac 1200

tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
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gagacctact gggtgcatt ctccagacgt ggaggcattc taagtcacag 2400
gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450
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gccacgagag tgacctctg tgcctctac tgcacactc ctgacagcac 2550
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cccaaaaggg ggaqqaatga ataattccac ccttgtttag caaataagca 2650

agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2706
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750
 tcaccttaaa aaaa 2764

<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259
 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
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 20 25 30
 Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp
 50 55 60
 Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr
 65 70 75
 Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe
 80 85 90
 Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile
 95 100 105
 Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val
 110 115 120
 Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe
 125 130 135
 Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp
 140 145 150
 His Arg Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly
 155 160 165
 Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro
 170 175 180
 Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu
 185 190 195
 Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys
 200 205 210
 Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro
 215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Ile Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggctctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

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<210> 263

<211> 357

<212> DNA

<213> Homo sapiens

<400> 263

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caacagaaaa ctctcaaaac aaaaaagttc agcagagagc ggcctctcat 150

ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcate acatcggcca gctaagatct gatttagaca 250
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<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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				20					25					30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
				35					40					45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
				50					55					60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
				155					160					165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
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Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln	350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr	365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly	380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg	395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly	410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp	425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln	440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp	455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu	470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp	485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser	500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln	515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu	530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn	545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln
				575					580					585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala
				590					595					600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr
				605					610					615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys
				620					625					630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly
				635					640					645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg
				650					655					660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser
				665					670					675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro
				680					685					690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu
				695					700					705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr
				710					715					720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser
				725					730					735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu
				740					745					750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly
				755					760					765
Ser	Ala	Val	Gln	Ser	Asn	Asn								
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<210> 265

<211> 249

<212> BNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

caactacgtt attacaccaa aagttaaaaa caatcatggt tcttgaggaa 50

aa 100

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
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Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
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Val

<110> 271

<111> 564

<112> DNA

<113> homo sapiens

<120>

<121> unsure

<122> 21, 69, 163, 434, 436, 444

<123> unknown base

<400> 271

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ctccctatgc tggcgcacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccongctgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatggtggt tggcactctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaanonttca acanttctat 450
 gacctatga cccagtcaa tgccaggtae gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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 acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtctgcgtg 200
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 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcacc 300
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 gaag gctt ggaagagat gaggtggaga aatcgagat ggtgtg att . . .
 agggggcgga tttttctct tgcaggtctg gttatcttag ttgcacacag 400
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<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

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cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgetgaatct gngcagcaca ttgcagcaac ccttgccctg atggtggttg 250
gcctcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattggggggc gcgatatttc ttcttgacgg tctggctatt tnnngttgcc 400
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<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctccct cctggatgga tgcgccacc gtcacattgc ctccccccan 50
tggaggaattt actcctatgc tggcgacaa atcctgaccc cccaggccat 100
ttaccgaagg gctttggatg tcttgcctgt tggagagaa cgggcagatc 150
ccattgcaaa ctctttgaat ccttgetgaa tctgagcagc acattgcaag 200
caaccogtgc cttgatgggg ttggcctcct cctgggagtg atagcaacct 250
ttgtgaccac cgttggcatg aagtgtatga agtgcttggg agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350
caggtctggc ctttttagtn ggcacagat cctatggcaa tagantntt 400
cnnnnntct atgacctat gaccccagtc aatgocaggt acgaatttgg 450

tcaggctctc ttcactggct gggtgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgcccttg aaggtgggtg ncatcccccc 100

tgggagtgaag tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

atgcataatt tcttcttaca gctctageta ttttagttnn cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gacctatga cccagtcaa 300

tggcaggtac gaatttggtc aggtctctct cactggctgg gctgctgctt 350

ctctctgctt tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<410> 276

<411> 495

<412> DNA

<413> Homo sapiens

<420>

<421> unsure

<422> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<423> unknown base

<430> 276

agcaatgccc tgcctccagt ggaggattaa ttcttatgnt ggggacaaca 50

ttgtgaatgc ccaggccatg tccggggggc tctggatgta cggggtgttg 100

cagagcaccg ggcagatcca gtgcacaagtn ttgactctt tgcagaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgtttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgggatattt ctntttgcag gtctggctat tttagttgac acagcatggt 350

atggcaatag aatnqttaa gaattttatg acctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg cccatnttg ctgttctctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataaggggg gcgcgatatt ttttcttgca ggtntggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

cccagtcaa tgccaggtac gaatttggc aggctctntt cactggntgg 150

gtgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacnctat gctggcgaac aacatentga ccgccaggc catgtacgag 100

gggctgtgga atgtctgcg tgtcccagag caccgggcag atccagtga 150

aagtcttga ctcttgcgt aatctdaga ccacattga agcaacnta 200

cgtaaatat aattacata ctcttggag taatadcaat ctctgtggc 250

acatttaca taaaactata taaactact aaaaacacat aaggtacaa 300

agatgaggat ggctgtcatt gggggcgcga tatttctct tgcaggtctg 350

gtatttttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtaogaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcctctctc tgccttctgg gaggtgcct 500

aatttgcgtg tctgtcccc gaaaaacaac ctcttaccac cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
ggggggtgca gctgttgggc ttcattctgc ttcttgggat ggaatcggcg 50
ccatggtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gacncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgctgcagag caccgggcag atccagtga aagtctttga ctcttctgtg 200
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcctc 250
ttcttgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgttg gaagacgat aggtgcagaa gatgaggatg gctgtcattg 350
gggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactgg ctgggctgct 500
gcttctctct gccttctggg aggtgcctta ctttctgttt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgaagcagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gttgcacag tagcttttcg cgtctg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctgcgcg gcacgcggc ctgcctctg cctccgccc 50
ctgcgcctgc accgcgtaga cgcaccccc cctccagcgc gccaccccg 100
tagaggaccc cgcgccgtgc ccgcaccggt cccgccttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttccgc ccgggtgacc tctcaggggt 200
ctcccgcca aaggcgctcc gcgcctaagg aacatggcga aggtggagca 250
ggtcctgagc ctgcagccgc agcacgagct caaatccga ggctccctca 300
ccgatgttgt caccaccaac ctaaagcttg gcaaccgcac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaacac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacaaa acaccaataq tgtctaaqtc 700
tctgagttct tctttggatg acacggaag taagaagggt atggaagaat 750
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
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ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctggtggtt ttgttcttta tcttgggtgt aattattggg 950
aagattgctt tctagaggta gcatgcacag gatggtaaatt tggattggtg 1000
gatccaccat atcatgggat tttaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100
atgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200
ctttattaat gacaagggaa accatgagta atgccacaat ggcattattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgccctg tgggtgctggc ccttggggag 1350
ctggagccca gcatgctggg gaggcggtc agctccacac agtagtcccc 1400
acgtggccca ctcccgccc aggtgcttt cctgtctctt agttctgtcc 1450
aagccatcag ctccctggga ctgatgaaca gagtcagaag cccaaaggaa 1500
ttgcactgtg gcagcatcag acgtactcgt cataagttag aggcgtgtgt 1550
tgactgattg acccagcgt ttggaaataa atggcagtgc tttgttact 1600
taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650
tatttcagag atgtttaatg catatttaac ttatttactg ttttccct 1700
catgttttct tattgtcaca agagtacagt taatgctgag tctgctgaa 1750
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agaactgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ctttttttaa 1950
tgaagagtag tcagtcttct agattgtct tataaccact ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
agacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
gggaggggaa tagtagttgt ggggggggag caagggaaga gagaaactct 2150
tgggctcctt ttttattat tttttaaata tgggagggg tcttctgaa 2200
tgggctcctt ttttattat tttttaaata tgggagggg tcttctgaa 2250
tgggctcctt ttttattat tttttaaata tgggagggg tcttctgaa 2280

<110> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Gln Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Thr Ile Val Gly Val Ile Thr Arg Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

gtcagtccttc tagattgtcc ttatcccacc ttccaaccan tactcacatt 50
tenagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaaag gccattttaa accattggta ggccctggta catgatgctg 50
gattacctcc ttaaatgaca centtccctg cctgttggtg ctggccnttg 100
cggagctgga gcccagcat gctggggagt gcggtcagct ccacacagta 150
gtcccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactctgcca gcatcagacc tactcgtcat aatgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgttt 350
gttcaactta aqqaccaa qctaaattgta ttggttcatt tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450
tcattctatg tttcttatt gtcacaagag tacagttaat gctcgcgtgc 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
ccctgggtggt tttgttcttt aattcggttg tgtaattntt gggaagattg 50
ctttagagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
ggtggcccat tcccggccca ggctgctttc cggtnctcag ttctgtccaa 50
gcaatcagct ccttgggaact gatgaacaga gtcagaagcc caaaggaatt 100
gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgctt tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gttaaagca tatttaantt atttaatgta tttnatntca 300
tgtctcttta ttgtcacaag agtaacgita atgctggctg ctgctgaant 350
ctcctgggtg ccttgggaatt gttgtgagct gttgtgaa cttctctctt 400
cttgatgctc tttctatgta ggggttga 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gtcttcagtt ctgtccaaag catcagctcc ttgggaattg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagaag 100
 tactgtcat aagtgaagg cgtgtgtga ctgattgacc cagcgctttg 150
 gaaataaatg gcagtgcctt gtccacttaa agggaccaag cttaaattgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacattaa aagttgaggg gaaaagattg atctcttctt aatgacaagg 50
 gaaaccontgn gtaatgcac aatggcatat tgtaaattgc attttaaaca 100
 ttggtagggc ttggtacatg atgctggatt acctctctta aaatgacacc 150
 ctccctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatget 200
 ggggagtgcg gtctgtcca cacagtagtc ccangtggc ccantcccg 250
 ccaggtgc tttcgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttggaaa taaatggcag tctttgttc anttaaaggg nccaagntaa 450
 atttgattg gtccatgtg tgaagtcaaa atgtattca gagatgttta 500
 atgtatatt aaattatca gaaagatca tttctgtt accatattgt 550
 aggggtg agtgaatg ttgtgtgtgt gaattatg ttggagaattg 600
 gtattgtg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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 cacagtagtc cccacgtggc ccactcccgg cccaggtgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggg 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aacaccaga gccagagcc ggg 23

<210> 294

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

caggggaatc atcgatgcag gggccccaat caatgatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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ggctgggtga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300
atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350
attttatgtg gcacttgaga aaggtagccc ggattgtcag tgaaaggact 400
ttccatctca ccagcccgcc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcctcgaat gccagaaaaga actcccaact cccagccttt 500
ctgaattgga ggattatctt tccatgaga ctgtctttga gaatggcacc 550
cgaaacttaa ccagggtgaa agttcaagat ttggtcttg agccgaactca 600
aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650
gcaccgacag caggttcagc atcttgaca aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
ttccctcag catgttctaa ctgctgccc ctgtgttcat gatggaaagg 800
actatgtcaa agggagttaa aagctaaggg tagggttgtt gaagatgagg 850
aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagagggtac cagagagcat ctgcaggaga 950
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tcgaagggc tgggacgag gagccatgg aaacctacc ttggaactatg 1100
actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150
cttggaatca gcccacgat caagaaaatg cctgggtggaa tgatccactt 1200
ctcaggattt gataacgata gggctgatca gttggtctat cggttttgca 1250
gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300
tcaggctcca ccagttcggg ggtctatctg cgtctgaaag atccagacaa 1350
aaagaattgg aagcgcaaaa tcattgggt ctactcaggg caccagtggg 1400

	20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu	35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr	50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu	65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn	80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu	95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg	110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp	125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu	140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu	155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly	170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser	185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala	200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu	215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln	230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys	245		250
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp	260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Ile Lys Arg Ala	275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys	290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp			

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	
365	370	375
Val Asp Val His Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggagggc cttcctttca gtggaccagg gtcaagaata cccag 41

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Gln	Gln	Gln	Asp	Asp	Lys	His	His	Gln	Ala	Ala	Arg	Arg	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Tyr Gln Ile Met Arg Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
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<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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ccagcggatg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
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<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25				30	

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35					40				45	

Val	Leu	Ile	Ile	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50					55				60	

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65					70				75	

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80					85				90	

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304
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 <212> DNA
 <213> Homo sapiens

<220>
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<223> unknown base

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tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
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attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgitt ggtgittgtg 500
tggaaaattat ctgcoctgggt t 521

<210> 305
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 305
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<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
accatgaca ccaaattgaa gaattca 26

<210> 307
<211> 45
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307

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<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

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actgcacaga gaattccatc atggacctga cccaactgat acagcccag 1250

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48

<223> unknown base

<400> 310

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caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

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cggagcccaq ccccttctca acccaaccca acctagcccn gtcacagcng 150
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atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
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caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
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<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

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<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 314

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<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

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<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 316

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<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

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<210> 318

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 318

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<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 319

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<210> 320

<211> 46

<212> DNA

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<400> 320

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<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

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gcatttgatg agctgaagac tgattacaag aatcttatag accagtgtaa 150
taccctgaat ccccttgtac tcccagagta cctcatccac gctttcttct 200
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tttttttact acctatatgg catgatctat gttttgggtga gctcttagaa 450
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tgaacgatt ctatcagca aatctctgt caagattatg ctatggaatc 550
tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttcacat 600

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<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactccca gactacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
atgagtggcc caggactctc tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300
tagcattttt ttactacctc tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttgggtccagt taagtgcagc caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgac agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 324

g a a a c c a c c g g g c a g t t a a a l a g a t t g t a a t a t a a c c t 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 325

c a g g a a a c a g c t a t g a c c a c c t g c a c a c c t g c a a a t c c a t t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
atgggaccaa ttctttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggcgcaaatt tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
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tgaacaaact gggactccca cccctctctg tcttaacat ggcctggccc 150
ggaagttccc gaaccattc gactgaagca ttgactcgg tcttgggtga 200
taccggctct taccaccagg cctgtcagtt gacctaccc ttgcacacct 250
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atggttgcca tcttgggttc cagaatcaga tgcatttcg tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttccctct 500
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
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 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttgct gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggoot taagaaatca ctataaaatg 1150
 caaataaagt tactcaaate tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20					25					30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35					40					45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Ile	His	Thr
			50					55					60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65					70					75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80					85					90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95					100					105	

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 310

<212> DNA

<213> Homo sapiens

<400> 331

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ggctgttttc aatttgtcag ttgtgggatg atggaattga cttaaatcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
 aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
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<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
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 aacagcaac aagctgagct gctgtgacag agggaaacaag atggcgqgcg 100
 nga-gggagc ctttggqlaa gacccaaact ggggclccc gggctgtgcg 150
 tgcagaccat ggcttggcc ggaggttcgg ggaccgcttc ggctgaagca 200
 tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct acctaaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
 gacttaaate gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcacaatct gatgagcaat atgcttgcca tcttgggttc cagaatcagc 450
 tggcatctgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tcttctctct aactctgggt aggtcattct ggagtgcacat 550
 gatgactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 334

tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg cgggaggttc ggggaccgct tcggctqaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

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gggcccggag gtggggcgcc gctggggcgg gcccgcaagg gcttcacatg 100
agggcgcacg gcccgcgacc gagecgtgagg actggcctcc caagcgtggg 150
gggacaagct gccggagctg caatggggcg cggctgggga ttcttgtttg 200
ggtccttggg cgcgtgttg ctgctcagct cggggccagg agaggagcag 250
cccgcggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
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tataaggtta acctgaagag ggcctatctt ttctgtaata acatcaccac 450
gttttcaaaa aggcactctc ctgtcaaaac atgtcaatct gatgaagttc 500
ctaatgcaat taaatctcgg agctacaagc attctgaaga agccaatgat 550
ctcattgaag aatctcaaca agctcaacga ctttgaagcag tgaatgaata 600
tcgaggtgag gaaacacaga aggtgtgtct tcagtgagcc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc cccgaagct 700
aatatctag atttctctct taactctcag agctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggttc tggtaagg 850
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatctt ctctacttaa 1100
 tagaactaag ggctttatcc aaagtgttac cattcttoga gcgccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
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 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaaact 1550
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtataag taatacttta ataattgtgt 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<100> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

<400> 337
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val
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 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp	35	40	45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg	50	55	60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg	65	70	75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln	95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu Phe	245	250	255
Ala Ser Ile Asn Val Phe Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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nacaacttttt acagttggct aaaaagttct tgtgtagaaa aaagagcatt 150
ctacagactt atatctdccc tacatgcaag cattaatgtg catttgactg 200
caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaa 250
attacagaat ttnaacagcg atttgatgga atttgactg aaggagaagg 300
tccaagaagg cttaagaact tgtattttct ctacttaata gaactaagg 350

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ctttatccaa agtggtacca ttcttngagc gccagattt tcaactnttt 400
actggaaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcac ttcttttgc ttttgatgag aattcatttt 500
tttggtg 507

<210> 339
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
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<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgctttotta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac ttctgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

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<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

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cactcacctg ttcttgcgcc tgggtgttct gacaggtctc tgcctccct 200
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tgagctaaag agagggtggg ggcagtgtct ctgaacatcc ataaaaaaa 550
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gtgcctctgc actctagcgt gggtagacaga gtaagcgaga ctccatctca 1300
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaagagacc catctctaaa taaatgtttt aaaaat 1486

<210> 346
<211> 124
<212> PRT
<213> Homo sapiens

<400> 346
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Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
20 25 30
Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
35 40 45
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
50 55 60
Leu Asp Asp Gly Pro Ser Gly Arg Arg Arg Gly Asp Val Tyr Arg
65 70 75
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
80 85 90
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
95 100 105
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
110 115 120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
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ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
ggcatggaac tccccttctg cactcacctg ttcttgcccc tgggtgttct 200
aacaggtctc tgctccccct ttaacctgaa tgaacatcac caacgcctat 250
tcccagggcc accagaaagc aaatttggat acagtgctct acaacatgtt 300
gggggtggac agcgatggat gctgggtggc gccccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgctg cctgtaggg gggggccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
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tggatgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 348
caggtgcata ttcacagcag gatg 24

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
tgaactcccc ttctgcactc acctgttctt gcccctgggtg ttctt 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
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gttctctggg cggctcttag aacaattcag gcttctctgc gactcaagcc 150
tcagctccaa catatgcatt ctgaagaaa atgctctaaa tctatagaa 200
gctttatatt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
tctgctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450
gtgaatacc agggggagta cgagagcctg tacacagacc acatctggat 500
ccccagcagc tgggtgtcac tcaactgaagg tctgagtggt gatgtcactg 550
atgacatcac ggccactgtg ccatacaacc ttctgtctag ggccacattg 600
qgctcacaga cctcagcctc cagcatctc aagcatctt ttaatagaag 650
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gctactgga ggagggagcc tgggtccagc caaatctca aatttgtgag 800
gagtgggggt attcagtgcc acctagaaac catggagcca ggggtgcat 850
actgtgtgaa ggcccagaca ttctggaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt agagctcaa ggagaggcca ttccctgggt 950
actggccctg ttgctttg ttggcttcat gctgacatt gtggctgtgc 1000

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctggtgcccc 1050
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 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
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 gtaacatgtg catgtttgtt gtgtctcttt tttctgttgg taaagtacag 2000
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 aaaaaa 2056

<210> 451

<211> 311

<212> PR1

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
					20				25					30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Ala Leu Gln Tyr Ser Lys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcctt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
tcattgtggt tttctacgca ttgattccat gtttgcctac agatgaagtg 300
gcattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcattctctg atgtggagcc cagtgatgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacata 450
tggtatccca gcagctggtg ctcactcact gaaggctctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagaa tctgaagca tccctttaat 600
agaaactcaa ccatccttac ccgaactggg atggagatca ccaaagatgg 650
cttnacactg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
taaccacat actcaatata gacgaantgc tattctccac ctatcttgagt 850
gggctgggt cgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcgccacgcg tccgagggac aagagagaag agagactgaa 50
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agaggcagga gctggaaagg agagaggag gaggaggagg agatgcggga 200
tgagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
aqaqgaqgtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
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augagtgggt ttgaaggggg gatctcagtc cctgggtgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtccctggag 500
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550
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cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650
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 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

1 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20						25				30	

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35						40				45	

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
			50						55				60	

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gectctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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ccgcacgcct ccgcaccca gctcgttctg tctcccccgc cctcgtcctt 100
gcagctactg ctacagaaacg ctggggcgcc caccctggca gactaacgaa 150
gcagctcctt tcccaccca actgcaggta taatttttga cgttttgctt 200
gcttttga ccagggttgag ggagcgcgag agggcggagg tgcgttatct 250
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atcctgaggt ctttcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550
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agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000
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 aaatgtattg tgctttgata ctaaaaatct gtaaaatgtt agttttggta 2950
 attttttttc tgctgggtgga ttacatatt aaattttttc tgctgggtgga 3000
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
				185					190					195			
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
				200					205					210			
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Gln			
				245					250					255			
Thr	Asn	Gln	Ile	Leu	Arg	Gln	Gln	Ser	Leu	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
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<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

100 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
ctccactcca gcatatactc ctac 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
acqaaagaaa gggagagagc caagcagagg ccacagacag ccttgggcat 50
ccacagaggg agcagcggga gacagcagag cgggaaggcc cggcccgggc 100
agagaaagcc gagcagagct ggggtggcgtc tccggggccc cgtccgacg 150
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<210> 370
 <211> 111
 <212> PRT

<213> Homo sapiens

<400> 370

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				20				25					30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35				40						45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50				55						60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65				70						75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80				85						90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
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Arg	Arg	Val	Tyr	Glu	Glu
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<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

ccagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

cccccaatggc caggagatt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373
ctccggtcag catgaggctc ctggcggecg ctgctcctgc tgetg 45

<210> 374
<211> 3113
<212> DNA
<213> Homo sapiens

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caaaatccgg ggctaagaa caccgttacc caatgagatc ttgggtccag 200
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 taagagactt tgt 3113

<210> 375
 <211> 816
 <212> PRT
 <213> Homo sapiens

<400> 375
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 Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn
 20 25 30
 Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
 35 40 45
 Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala
 50 55 60
 Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro
 65 70 75
 Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val
 80 85 90
 Lys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu
 95 100
 Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val
 110 115 120
 Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro
 125 130 135
 Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr
 140 145 150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser	155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly	185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	245	250	255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	335	340	345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	365	370	375
Gln Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	425	430	435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
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His	Ser	Thr	Thr	Arg	Val									
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<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377
 aacccccgag ccaaaagatg gtcac 25

<210> 378
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 378
 gtaccgggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379
 <211> 2461
 <212> DNA

<213> Homo sapiens

<400> 379

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 ggcctcactc g 2461

<210> 380
 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 380
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 Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu
 20 25 30

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				35					40					45			
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro			
				50					55					60			
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met			
				65					70					75			
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp			
				80					85					90			
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe			
				95					100					105			
Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln			
				110					115					120			
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr			
				125					130					135			
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys			
				140					145					150			
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu			
				155					160					165			
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn			
				170					175					180			
Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr			
				185					190					195			
Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp			
				200					205					210			
Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met			
				215					220					225			
Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val			
				230					235					240			
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser			
				245					250					255			
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asp	His	Arg	Val	Ile	Gln	Leu	Tyr			
				260					265					270			
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu			
				275					280					285			
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro			
				290					295					300			
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe			
				305					310					315			

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
320 325 330

Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
335 340 345

Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

ccttggtcg tggcagcagt gg 22

<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

caactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacggt cgagtacttg aaacqggagc actcgctgtc gaagc 45

<210> 384

<211> 2050

<212> DNA

<213> Homo sapiens

<400> 384

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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25				30	

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40				45	

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55				60	

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
				140					145					150

Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Arg	Ile	Tyr	Ile	Tyr	Tyr	His	Gly	Leu	Leu	Ile	Asn	Asp	Arg
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asn Ala Cys His Arg Gln Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

ccaagcagct tagagctcca gacc 24

<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct qtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50

cctttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100

atcctttctg ggagttcaag attgtgcagt aattgggttag gactctgagc 150

gcccgtgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

cacgcgcctg aagcacaaaag cagatagcta ggaatgaacc atccctggga 250

gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300

gggcgaagga actgctcctg acttcaqtca ttaagggcac aattgaaaat 350

aatttggag gaagatcaga ctgattcctg cgggactgca cgggactac 400

aaagggttg tctgtctggg aatctcctg gggactctgt gggagaccgg 450

atgcacccag atagctatt cagttccgga agagctggag aaaggctcta 500

gggtggggga catctccagg gacctggggc tggagccccg ggagctcggc 550

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<210> 390
 <211> 916
 <212> PRT
 <213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu			
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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln			
			20						25					30			
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val			
			35						40					45			
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala			
			50						55					60			
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe			
			65						70					75			
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile			
			80						85					90			
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn			
			95						100					105			
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu			
			110						115					120			
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Gln			
			125						130					135			
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met			
			140						145					150			
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn			
			155						160					165			
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu			
			170						175					180			
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val			
			185						190					195			
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu			
			200						205					210			
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Ala	Thr	Gly	Thr			
			215						220					225			
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro			
			230						235					240			
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu			
			245						250					255			
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp			
			260						265					270			
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp			
			275						280					285			

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Ile Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Gln Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Phe Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
				905					910					915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

ttcgtctctg tgaacggcc cac 22

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcggggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccactatga caggagc g agtaca ttgttcac 4

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggtct agtgcaggac gagaaggagg aggaacagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgogg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550
 aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600
 acccagcctg gccagaagtg caccgtctca ggtgggggca ctgtcaccag 650
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 tccccagaaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
 atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800
 tggaggcccc ctggtgtgtg atggtgcact ccagggcata acatcctggg 850
 gtcagacccc ctgtgggagg tccgacaaac ctggcgtcta taccaacata 900
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

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Leu Leu Leu Gly Gly Ala Thr Ala Gly His Ser Arg Ala Gln Gln
 20 25 30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
 35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
 50 55 60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
 65 70 75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> RNA

<213> Artificial Sequence

<220>

<221> Synthetic nucleotide sequence

<222> 396

gagctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gcccccgccc gggcccgccc ccgcgcgcgc gccaggtga gcgctccgcc 150
cgccgcgagg ccccgccccg gcccgcccc gccccgcccc ggccggcggg 200
ggaaccgggc ggattctctg cgcgtcaaac cactgatcc cataaaacat 250
tcatactccc ggcggcccgc gctgcgagcg ccccgccagt ccgcgcgcgc 300
gcgcgcctcg cctgtgcgc cctgcgcgc ctgcgcaccc gcggcccgag 350
ccagccaga gccgggggga ggcgagcgcg ccgagcctcg tcccggggcc 400
gggcgggggc cgggcggtag cggcgggccc tggatgcgga cccggccgcg 450
gggagacggg cgcgcgcgcc gaaacgactt tcagtccccg accgcgcgcc 500
cccaacccct agcatgaaga ggcgcgcgc tgcgcgcgc cgcgcgcgc 550
catcctatct atcctatcag cctcgcgcgc tgcgcgcgc cgcgcgcgc 600
cctcctatct atcctatcag cctcgcgcgc tgcgcgcgc cgcgcgcgc 650
cctcctatct atcctatcag cctcgcgcgc tgcgcgcgc cgcgcgcgc 700
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gcgataatgc acagctccgc tctgtggacc ctgcacatt ccacggcctg 900

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 aactctatc tgtttgcaa caatctatca gcgctgccc ctgaggccct 1250
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 ttacagggtt cggcggcagc gtttgttcca gaacgcgcgc tcccaccag 2150
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 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
			50						55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	Phe	Thr	His	Ala	Ala	Ala	Ala	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val
275	280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg
290	295	300
Leu Ala Ala Asn Asp	Leu Gln Gly Cys Ala Val Ala Thr Gly Pro	
305	310	315
Tyr His Pro Ile Trp	Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu	
320	325	330
Gly Leu Pro Lys Cys	Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly	Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro	Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn	Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu	Thr Ala Val Arg Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr	Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr	Arg Ser His Cys Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly	Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys	Ser Leu Thr Pro Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu	Gly Pro Cys	
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtaacct tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<213> Synthetic oligonucleotide probe

<400> 402

cctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agctcagat actggggact ttacagtcac acagaaccgt cctcccagga 150
agetgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
aaaaggcaag tcttttttct ctttctcctt ttgggcttat ctctggcggg 250
cgcgggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaaattc 350
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<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20						25					30
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
			35						40					45
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Gln	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Gln	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Gln	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440		445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455		460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470		475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485		490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500		505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515		520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530		535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545		550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560		565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575		580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590		595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605		610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620		625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635		640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650		655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665		670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680		685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695		700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710		715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatc ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagtgtctc cattcaggag gatctacct tctctctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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 gcgtagccgt gcgcgcattg cctctcgcc tgggcaatgg tcccggtgc 100
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 tgctgtgggt gctgggactt cccgcgcgc gcgtggaggt tgcagaggaa 200
 agtggtcgt tatggtcaga ggagcagcct gtcacccct tccaggtggg 250
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 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agcctttct ctctggatgg cgtggagca 500
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<211> 360
 <212> PRT
 <213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu	1	5	10	15
Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	20	25	30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	35	40	45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	50	55	60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	65	70	75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	80	85	90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	95	100	105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	110	115	120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	125	130	135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	140	145	150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	155	160	165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	170	175	180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	185	190	195	
Ser	Gln	Asn	Leu	Met	Arg	Thr	Leu	Ala	Val	Asp	Gly	Ser	Asp	Cys	200	205	210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	215	220	225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	230	235	240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	245	250	255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly				

	260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His	Thr Asp Arg Thr	Leu Glu
275		280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln	Thr Gly Ile Glu	Ala Lys
290		295	300
Lys Asn Val Val	Val Thr Gln Ala Asp	Gln Ile Gly Pro	Leu Pro
305		310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp	Leu Leu Val Phe	Ser Leu
320		325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr	Ala Thr Ile Arg	Thr Glu
335		340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln	Glu Gln Glu His	Val Glu
350		355	360

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgg cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggcgagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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1	5	10	15
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Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Tyr Val Ser Val Leu Trp Leu Tyr	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
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<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
 ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
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 cggctgggtgt tctgtctcgc gatnagcctg ctcaaactgtt ccaacgccc 150
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<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	1	5	10	15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	20	25	30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	35	40	45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	50	55	60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	65	70	75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	80	85	90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	95	100	105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	110	115	120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	125	130	135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	140	145	150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	155	160	165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	170	175	180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Gln	Asp	Ile	Pro	Leu	Met	185	190	195	
Leu	Gly	Val	Trp	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	200	205	210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	215	220	225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	230	235	240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	245	250	255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp	410	415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser	425	430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln	440	445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly	455	460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala	470	475	480
Gly Val Leu Gly	Phe Ser Thr Ala Thr	Ile Leu Cys Val Ala Arg	485	490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His Pro	500	505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr	515	520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala	530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag cctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggttcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtacacata ctgttctatc gggtaggtc cctctttagc cagctctgt 50

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tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly
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Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Val Val Leu Val Leu Val Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Ala Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn
320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val
335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro
350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu
365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His
380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr
395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg
410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln
425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile
440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr
455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile
470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val
485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile
500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr
515	520	525
Gln Gln Met Ala	Gly Phe Glu Phe Gln	Val Ile Arg Glu Asp Ser
530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu
545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu
560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr
575	580	585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro	590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro	605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala	620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His	635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val	650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile	665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu	680	685	690
Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser	695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile	710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu	725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr	740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg	755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val	770	775	780
Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Ile Thr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	860	865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Ihr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Ile Ala Ser Ile Ile Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggaacatt cagtattgat gccaaacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

ggagcgcctg aacaaagggg tgggggagc ggggggagc 50

cctgggagaa gccagaccgt gtaagggagg ctgtggggag agcgtgctgt 100

ggcctcqqaa agtgggaagt ggaggcagaa gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctccca gatactatct 200

tttggatttg ggtggctttt ctccatgggt caattgttta aagactatga 250

gatacgtcag tatgttgtac aggtgatctt ctccgtgacg ttgtcatttt 300

cttgaccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met	Ser	Phe	Leu	Ile	Asp	Ser	Ser	Ile	Met	Ile	Thr	Ser	Gln	Ile
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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120
Met	Tyr	Phe	Phe	Trp	Tyr	Leu	Gln	Asp	Ile	Ile	Leu	Leu	Leu	Ser
			125						130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
			140						145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
			155						160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
			170						175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Ala Thr Ile	Ile Thr Ser Ser Ser	Gly Val Leu Gln Thr	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
	440	445	450
Lys Gln Met Ala	Pro		
	455		

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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ttgtacnggt gatcttctcc gtgacgttg ccattttctg caccatgttt 200
gagctcatca tctttgaaat cttnngagta ttgaatagca gctcccgta 250
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tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
ataaacaac gactgcttt ttctgtctn ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgttg 200
ccattttctg caccatgttt gagctcatca tntttgaaat nttaggagta 250
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tgagcaatat ccgactactg ataaacaac gactgcttt ttctgtctn 400
ttatggctga cctttatgta ttntnttgg aaantaggag atccccttcc 450

cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tggttgttta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgttgtacag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

ctcgcgacagg gatcgctccca tggccgggggc tgggagcgcg gacccttggg 50

gggcttcagg gatctgctac ctttttgggt cctgtctcgt cdaactgctc 100

ttctcagggg ctgtcgccctt caatctggac gtgatgggtg ccttgccgaa 150

ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccacag agctggctgc tggtaggtgc tcccaggcc 250

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<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30

Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45

Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
														60

Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75

Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
				80					85					90

Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
				95					100					105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly
680		685 690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro
695		700 705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met
710		715 720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro
725		730 735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val
740		745 750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr
755		760 765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr
770		775 780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu
785		790 795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro
800		805 810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser
815		820 825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val
830		835 840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln
845		850 855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro
860		865 870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val
875		880 885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser
890		895 900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg
905		910 915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu
920		925 930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu
935		940 945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn
950		955 960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

122

<223> Synthetic oligonucleotide probe

<400> 438

gggagacacc gcagtgcctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

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<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ggagctgcca gcacagtgtt ggctcacaac aagatgtcca aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcgccgggt ggtgcagcc gggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

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<210> 442

<211> 436

<212> PPT

<213> Homo sapiens

<400> 442

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Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25						30

Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
			65					70						75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
			80					85						90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
			95					100						105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
			110					115						120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
			125					130						135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
			140					145						150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
			155					160						165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
			170					175						180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
			185					190						195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
			200					205						210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
			215					220						225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
			230					235						240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
			245					250						255					
Met	Phe	Asn	Arg	Leu	Arg	Thr	Leu	Thr	Asp	Leu	Leu	Leu	Leu	Asp	Gln				
			260					265						270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
			275					280						285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
			290					295						300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
			305					310						315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

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<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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<210> 447

<211> 229

<212> FRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20				25						30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35				40						45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50				55						60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

...agagaggg agggagata aga aa

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50
agcataccag atctcaccag agagtgcag acactatgct gctcccatg 100
jccctgccca gtgtgtctctg gatgctgctt tcttgctca ttctctctg 150
tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200
gtgtgcccaa aggtcccaag gctatggct cccctgcta tgccttgttt 250
ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300
ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tcttctgtgt 350
cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400
ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450
gagtagcaat gatgtgatga attactttgc atgggagaaa aatccctcca 500
ccatctttaa ccttgccac tgtgggagcc tgtcaagaag cacaggattt 550
ctgaagtgga aagattataa ctgtgatgca aagttaccct atctctgcaa 600
cttcaaggac tagggcaggt gggaaatcag cagcctcagc ttgggtgca 650
gtctatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700
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gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850
aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
			20						25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
			35						40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
			50						55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
			65						70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
			80						85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
			95						100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
			110						115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
			125						130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
			140						145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
			155						160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
			170						175						

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

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tgggtgtgaga gcacagagga gtgggcccggg accatgcggg ggacgcggct 100
gggtctctctg ggcctgggtgc tgggtgcctg cggagagctg ggcgccggccc 150
tggcctgtcta cgtctgtccg gagcccacag gactgtcgga ctgtgtcacc 200
atgcgccact gcaccaccac cgaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccctc tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccg 400
tetgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
tccgactgta gagtccccgc ccacccccat ggccttatgc ggcccagccc 500
cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454
Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
1 5 10 15
Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
20 25 30
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 1518
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455
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agccgaaccg gcaagggttc gtggggaacc aggcttgcaa agtgacggtc 100
attttctctt tctttctccc tcttgagacc ttctgagatg atggtctctg 150
gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggccgctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctggcgggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgcggg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccogt gcgcagagga 400
 cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450
 acgcaggcgt gcaaactctgt ctgcctgca ggaagcgccg aaaacgctgc 500
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600
 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750
 tctggtccaa gatctgtaaa cctctcctga aagaaggcca agtgtgtacc 800
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850
 ctgtggagaa ggtctgtctt gccggataca gaaagatcac catcaagcca 900
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
 acattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100
 ttatggaaact cccctgtgat tgcagtaaat tactgtattg taaattctca 1150
 gtgtggcaact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200
 aatgctgcac tgccatattt tccctctgtt atgtaaattt ttgtacacat 1250
 ttgattgtat ttgattgac aaatattcta tattgaactg aagttaaaca 1300
 tttcagotta tagttcttaa aagcataacc ctttaccoca ttttaattcta 1350
 gagtctagaa cgcaaggatc tcttggaatg acaaatgata ggtacctaaa 1400
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500
 ttttaaaaaa aaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

Met	Met	Ala	Leu	Gly	Ala	Ala	Gly	Ala	Thr	Arg	Val	Phe	Val	Ala	
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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser	
				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
				260					265						

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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catttttttt tctttctcct tenggagtc ttntgagang atggtttttg 150
gcgagcgggg agctaaccgc gttttttgtn gcgatggtag cggcggtttt 200
cggcgggcac ctntgtctgg gagtgagegc caccttgaat cggttttcaa 250
ttccaacgnt atcaagaacc tgcccccacc gntggggggc gctgcggggc 300
accaggnnt tgcagtcagc gccgcgcggg gaatcctgta cccggcgggg 350
aataagtacc agaccattga caattaccag ccgtaccgt gcgcagagga 400
cgaggagtgc ggcactgatg agtactggc tagtcacc cgcggagggg 450
angcgggcgt gcaaantgt ntngcctgca ggaagggcg aaaacgctgc 500
atgcgtcang ctatgtgctg cccgggaat tactgcaaaa atggaatatg 550
tgtgtnttct gatcaaaatc atttcggagg agaaattgag gaaaccatca 600
ctgaaagctt tggtaatgat catagcact tggatggg 638

<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

100 458
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ttctctcttg caecgggtgc ttgggctcgg ccaggcgggg tccgcgcga 150
gggtttgagg atgggggagt agctacagga agcagccccg cgatggcaag 200
gtatatTTTT gtggaatgaa aaggaaatat taataatgag ctgaaganna 250
ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcaccct 300

tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350
accagcagtg aatcttaatg ttcacttaaa tcagaacttg cataagaaaag 400
agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450
gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500
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gaaataagac aagctttcaa gaaattggca ttgaagttac atcctgataa 600
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ggagaaaagg gacttgagga taatcaagggt ggccagtatg aaagctggaa 750
ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800
cattggaaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850
tttgtaaatt ttiactcccc aggctgttca cactgccatg atttagctcc 900
cacatggaga gacttgcta aagaagtgya tgggttactt cgaattggag 950
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ggtgtccacc atgtcgagct ttaactaccag agttacgaag agcatcaaat 1750

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tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900
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tggaactctt ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650
tgttgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700
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 aatgatactg tagttattcc agttactagt ttactgtcag agggetgcct 3800
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<210> 459
 <211> 747
 <212> PRT
 <213> Homo sapiens

<400> 459
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 Arg Ile Ile Leu Cys Phe Leu Ile Val Tyr Met Ala Ile Leu Val
 20 25 30
 Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr
 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75

Asp Phe Leu Lys	Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys	Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly	Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile	Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe	Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr	Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg	Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val	Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn	Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala	Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				740	745	

<210> 460
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
 actcaccagc ctgttcacac tgcc 24

<210> 461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 461
 gatacagccag ccaataccag cacc 24

<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
 gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

agacagtacc tctctcctag gactacacaa ggactgaacc agaaggaaga 50
ggacagagca aagccatgaa catcactcta gaaatccttc tgcttctgat 100
caccatcctc tactctactc tggagtcggt ggtgaagttt ttcattcctc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300
agtgcgagaa actaggcgctc actgcgcctg cgtatgtggt agactgcagc 350
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtgggtga ataatgctgg gacagtatat ccagccgctc 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcaatt ctctcctaga tgatggagag 550
aaatcatggc cacatcgcca cagtggcttc agtgtgcggc cacgaagggg 600
ttccttaact catcccatat tgttccagca aatttgcgcg tgttggcttt 650
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700
aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750
caagcacaag attatggcct gtattggaga cagatgaagt cgtagaagt 800
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
tatcaatata tttctgagac tacagaagtt tttctctgaa cgcgcctcag 900
cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
aaaatcaaaa tgaaatgaat aaataagctc caccacagaa ctatgcctg 1000
ataatgatat gaatagtttc gaatcaatgc tgcaaaagctt tatttcacat 1050
tttttcagtc ctgataatat taaaaacatt ggtttgcccac taqcaqcaat 1100
caaacgaaca agattaatta cctgtcttcc tgttttctcaa gaatatttac 1150
gtagtttttc ataggtctgt ttttctttc atgcctctta aaaacttctc 1200
tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250
catttaaaag tggacaaaag ctactcctc aaagttaaat aaaaagagaa 1300
cttatttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatata aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
 attcagcatt tgaagattt ccctagcctc ttcctttttc attagcccaa 1500
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550
 aactctgaag tccacaaaaa gtggaccctc tatatttctt ccctttttat 1600
 agtcttataa gatacattat gaaagggtgac cgactctatt ttaaattctca 1650
 gaattttaag ttctagcccc atgataacct tttcttttgt aatttatgct 1700
 ttcatatata cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Leu	Ile	Thr	Ile	Ile	1	5	10	15
Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	20	25	30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90	
Ala	Val	Asp	Leu	Ser	Asn	Ala	Leu	Glu	Ile	Lys	Arg	Ser	Leu	Asn	95	100	105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly				

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly	His Glu Gly Ile Pro	
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe	Ala Ala Val Gly Phe	
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala	Leu Gly Lys Thr Gly	
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe	Val Asn Thr Gly Phe	
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro	Val Leu Glu Thr Asp	
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile	Leu Thr Asn Lys Lys	
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile	Phe Leu Arg Leu Gln	
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile	Leu Asn Arg Met Gln	
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His	Lys Ile Lys Met Lys	
290	295	300

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465
 tggcggcgccg tgcggggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50
 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccg 100
 gagagggccg agcccgcccg gggcaggatg accaaggccc ggctgttcg 150
 gctgtggctg gtgtggggt cagtggtcat gactctgctg atcatcgtgt 200
 actggaacag cgcaggcccg ggcgactct acttgacac gtccttctct 250
 aggcgcacac cggggcccgcc gctgcccacg cccggggcccg acagggacag 300
 ggagctcagc gccgactccg atgtcgacga gtttctggac aagtttctca 350
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
 cctgcgcccg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 ggcgcacgac cggccacccc cagaccagg cccgcagcac cccgagcgga 500
 ggagcgtgct ggggggcttc tgcgccaact ccagcctggc ctccccacc 550

aaggagcgcg cattogaaga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccattctactg ctacgtgccc aaggtggcct 650
gcaccaactg gaagcgcgctg atgatcgtgc tgagcggaag cctgctgcac 700
cgcggtgogc cctaccgga cccgctgcgc atcccgcgcg agcacgtgca 750
caacgccagc ggcacactga ccttcaacaa gttctggcgc cgctacggga 800
agctctcccc ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
ctcttcgtgc gcgacccctt cgtgcgcctg atctccgcct tccgcagcaa 900
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccacgc 950
tgcggtctga cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000
ttccgcgtg gctcaaggt gtcttcgccc aacttcatcc agtaacctgt 1050
ggacccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
tgtaccgct ctgccaccgc tgcagatcg actacgactt cgtggggaag 1150
ctggagactc tggacgagga cgcgcgcag ctgctgcagc tactccaggt 1200
ggacccgcag ctccgcttcc ccccgagcta ccggaacagg accgcacgca 1250
gctgggagga ggactgggtc gccaaagatcc cctgggctg gaggcagcag 1300
ctgtataaac tctacgagga cgactttgtt ctcttcggct accccaagcc 1350
cgaaaacctc ctccgagact gaaagcttcc gcgttgcttt ttctcgctg 1400
cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatitt 1450
gcaatctggg cttcttgctc actccactgc ctctatccat tgagtactgt 1500
atcgatattg ttttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
1				5					10					15

Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20						25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
					35				40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55					60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser	65	70	75
Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln	80	85	90
Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp	95	100	105
Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln	110	115	120
Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser	125	130	135
Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro	140	145	150
Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala	155	160	165
Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg	170	175	180
Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro	185	190	195
Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala	200	205	210
Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys	215	220	225
Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys	230	235	240
Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe	245	250	255
Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe	260	265	270
Ala Val Pro Met Leu Arg Leu Tyr Ala Arg His Thr Ser Leu Pro	275	280	285
Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe	290	295	300
Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu	305	310	315
Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His	320	325	330
Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu	335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg
				350					355					360
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser
				365					370					375
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln
				380					385					390
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr
				395					400					405
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp						
					410									

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
 tcggggccaga attcggcacg aqgcggcacg agggcgacgg cctcacgggg 50
 ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
 acgggatggc tacgggaacg cgctatggcg ggaaggtggt ggtcgtgacc 150
 gggggcgggc ggggcacggc agctgggacg gtgcgcgcct tcgtgaacag 200
 cggggcccgca gtgggttatct ggcacaagga tgagtctggg ggccggggcc 250
 tggagcagga gctccctgga gctgtcttta tctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct gggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400
 ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaacctc 450
 ctggggacgt acaccttgac caagctcgcc ctccctacc tgcggaagag 500
 tcaagggaat gtcacaca tctccacct ggtgggggca atcgccagg 550
 ccagggaat tccctatgtg gccaccaagg ggcagtaac agccatgacc 600
 aaagtcttgg cctgggatga aagtcctat gggtcccgag tcaactgtat 650
 ctcccagga aacatctgga cccgctgtg ggaggagctg gcagccttaa 700
 tcccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
 ggccgcatgg gccagcccgc tgaggtcggg gctccggcag tgttccctgg 800
 ctccgaagcc aacttctgca cgggcattca actgctcgtg acgggggggtg 850
 cagagctggg gtaagggtgc aaggccagtc agaacacccc cgtggacgcc 900

cccgatatcc ctctcctgatt tctcttcattt ctacttggggg ccccccctcct 950
 aggactctcc caccoccaaac tccaacctgt atcagatgca gcccccaagc 1000
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcaggttc 1050
 ccataaaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr
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Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn
				125					130					135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln
				140					145					150
Ala	Val	Pro	Thr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr
				155					160					165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn
				170					175					180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu
				185					190					195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met
				200					205					210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
 aggcgggag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccttgcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaaccgatat ccgcgatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgcaget gtggatgtcc aacaagagga gctgtctccc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcaag 400
 gtgcctgtgt ctgggtgtg tgaacccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgcgcctc 500
 tgcacgccac cgcacccgac agggccttgc cgcacagcgg cagtcatgga 550
 gaccatcgtc gtgggtgca cctgcattct ctgaatcac tggcccagaa 600
 gccaggccag cagcccgaga ccattctctt tgcacctttg tgcacagaaa 650
 ggcatatgaa aagtaaaccac tcaattttga aagcaag 687

<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
 1 1 1 15
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val	
				35					40					45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	
				50					55					60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	
				65					70					75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	
				80					85					90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	
				95					100					105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	
				110					115					120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	
				125					130					135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	
				140					145					150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	
				155					160					165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe	
				170					175					180	

<210> 471
 <211> 2368
 <212> DNA
 <213> Homo sapiens

<400> 471
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 ctcccgagc agaagctag ctaggagcc aaatggggg ggggggag 150
 ctcccgagc ctcccgagc ctcccgagc ctcccgagc ctcccgagc 200
 ctcccgagc ctcccgagc ctcccgagc ctcccgagc ctcccgagc 250
 ctcccgagc ctcccgagc ctcccgagc ctcccgagc ctcccgagc 300
 gctgaaattt ctcccgagc ggtgctgct ctcccgagc ctcccgagc 350
 aatgggagcg ttttgcaaag aatgggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcatccaaga accagcttct atgagccgct tatttgctac 450
 cactctccca gcatTTTTT atgcaaagga tgggatattc cgcggttate 500

gtggcccagg aatcttcgaa gacctgcaga attatatott agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatt 650
ttcacaaacta tttcacagtg actcttggaa ttctgtcttg gtgtttctat 700
gtgttttttcg tcatagccac cttgggttttt ggctttttta tgggtctggt 750
cttgggtgga atatcagaat gttctatgt gccacttcca aggcatttat 800
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctgggtgtg 1000
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
tgtgaccgg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
agcaaccctg ccagctgac acagaggtgg tggaagactc cttgaggcag 1150
cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200
caagaataca caccaaaaca atatgtcagc ttcccttgg cctgcagttt 1250
gtaccaaaatc ctttaattttt cctgaatgag caagcttctc ttaaaagatg 1300
ctctctagtc atttggctctc atggcagtaa gccctcatgta tactaaggag 1350
agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtgttgg 1400
gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450
agagtctoga ccagaggagg ccattcccag tctaattcag cactttccag 1500
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 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300
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 agggaggcta atttcttt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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Ala	Trp	Ile	Ala	Ala	Val	Ala	Ala	Thr	Ala	Gly	Pro	Glu	Glu	Ala
			20					25					30	

Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
			35					40					45	

Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
			50					55					60	

Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
			65					70					75	

Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
			80					85					90	

Val	Asp	Val	Ile	Gln	Gln	Pro	Gly	Leu	Ser	Gly	Leu	Phe	Phe	Val
			95					100					105	

Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
			110					115					120	

Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
			125					130					135	

Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
			140					145					150	

Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
			155					160					165	

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr	320	325	330
Glu Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala	335	340	345
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgacggctc caac 24

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<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

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ctctctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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<210> 477
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Met Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
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<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
gtccacagac agtcattctca ggagcag 27

<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
araagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
atctctccag agccatggta cctc 24

<210> 481
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
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<400> 481
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<210> 3819
<211> 3819
<212> DNA
<213> Homo sapiens

<400> 482
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tcttggtcca tctgaacctc cactctccgg gttcaagtga ttctcatgac 150

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<210> 483
 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser
 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Val	Gln	Val	Leu	Gln	Ala	Arg	Val	Leu	Gly	Gln	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val
380	385 390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu
395	400 405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val
410	415 420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg
425	430 435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu
440	445 450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro
455	460 465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile
470	475 480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu
485	490 495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr
500	505 510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly
515	520 525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp
530	535 540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly
545	550 555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser
560	565 570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn
575	580 585
Phe Ala Met Leu Ala Ser Met Val Val	Glu Thr Leu Arg Leu Arg
590	595 600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu
605	610 615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe
620	625 630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile
635	640 645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser
650	655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
 665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
 680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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gggtggccct gacaggctct gaaggetggc tgcgagacca gtgcacatt 200

cttgcacttc tctgtctcac ctgcttttcc tggatggggc togaggggta 250

caactctac cgaactgtgg tggaggtctt tggcaactat gtccctggt 300

acctactcaa gctgagcgcc atgggttggg gcttcacctat cttctgtgtg 350

agcttgggtg ccctgggtga tgtggacaac tatgggacca tcatcttggc 400

tgtgcatagg actccagagg ggtcatcta cccttcacatg tcttggatcc 450

gggactccct ggtcagctac atcaccaccc tgggctctt cagcctggtg 500

cttctgttca acatgc 516

<210> 485

<211> 517

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

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<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 486

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

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<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90
Asn	Gln	Arg	Phe	Gly	Leu	Ser	Asp	Pro	Gln	Asp	Asn	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Ile	Val	Gln	Val	Ser	Pro	Val	Val	Val	Val	Val	Val	Val
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

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<210> 492

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 492

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<210> 493

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 493

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<210> 494

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 494

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<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Ile	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Ile	Leu	Gln	Ile	Ile	Leu	Leu	Val	Pro	Val	Gly	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe			410
Gly Arg Ile Tyr Val Val Asp Leu Ser Ser Val Lys Ser Ser	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Lys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asn Val Ile Ile Leu Ile Phe	980	985	990
Leu Val Lys Pro Ser Ser Lys Val Tyr Thr Val Val Val Val	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
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<210> 497
<211> 4199
<212> DNA
<213> Homo sapiens

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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Arg	Leu	Tyr	Leu	Ala	Thr	Asn

Cys	Tyr	Phe	Asn	Lys	Val	Lys	Ile	Gly	Ile	Asn	Ile	Ser	Leu	Arg
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His	440	445	450
Ile Ala Lys Arg Arg Ser Tyr Asp Phe Gln Ile Asp Pro His Ser	455	460	465
Asn Ile Tyr His Phe Thr Arg Ser Asp Ile Glu Ile Asp Ile Ser	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys His Leu Asp Ile Ser Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Leu Asn Leu Thr Thr Asp Leu Leu Thr Thr Thr	755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Trp Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 499

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<210> 500

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 500

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<210> 501

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 501

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

<400> 505

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(1210) 506

(1211) 273

(1212) PRT

(1213) Homo sapiens

(1400) 506

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Ala	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Pro	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Leu	Ser	Gly	Arg	Leu	Ala	Trp	Gly	Leu	Val	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Pro	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

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Gly His Ser Leu Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys Gly		
170	175	180	
Gly Pro Pro Arg Val Ala Pro Asn Pro	Thr Gly Val Asp Ser Ala		
185	190	195	
Met Lys Glu Glu Val Gln Arg Leu Gln	Ser Arg Val Asp Leu Leu		
200	205	210	
Glu Glu Lys Leu Gln Leu Val Leu Ala	Pro Leu His Ser Leu Ala		
215	220	225	
Ser Gln Ala Leu Glu His Gly Leu Pro	Asp Pro Gly Ser Leu Leu		
230	235	240	
Val His Ser Phe Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser Glu		
245	250	255	
Gln Ile Ser Phe Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys Lys		
260	265	270	

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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<210> 508

<211> 508

<212> PRT

<213> Homo Sapiens

<400> 508

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Phe	Gly	Arg	Arg	Val
				20					25				30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Phe	Val	Ser	Glu	Ser	Phe	Val
				35				40					45	

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg	50	55	60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg	65	70	75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro	80	85	90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala	95	100	105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro	110	115	120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln	125	130	135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln	140	145	150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu	155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly	170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala	185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu	200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala	215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu	230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu	245	250	255
Gln Ile Ser Phe Leu Gln Gln Gln Ile Gly Ser Cys Ser Cys Lys	260	265	270

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 100

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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
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Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
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Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
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Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
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Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
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Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
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Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
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Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Ile	Lys	Gly
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Pro	Pro	Arg	Val	Ala	Pro	Asn	Ile	Thr	Gly	Val	Asp	Ser	Ala	
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				200					205					210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
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Ser	Gln	Ala	Ile	Glu	His	Gly	Leu	Ile	Asp	Ile	Gly	Ser	Leu	Ile
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<210> 515

<211> 564

<212> PRT

<213> Homo sapiens

<400> 515

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Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met

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Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu	50	55	60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu	65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp	80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile	95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln	110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile	125	130	135
Val Ivs Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro	140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe	155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn	170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr	185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser	200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr	215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val	230	235	240
Gly Leu Thr Tyr Ile Lys Thr Thr Thr Thr Thr Thr Thr Thr	245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val	260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asp Cys Cys Glu	275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly	290	295	300
Ile Leu Pro Leu Glu Gln Ser Gly Ser Arg Pro Pro Ser Thr Gln			

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<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtgaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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<210> 523

<211> 344

<11> FRT

<213> Homo sapiens

<400> 523

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			20						25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
			35						40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
			50						55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
			65						70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
			80						85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
			95						100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
			110						115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
			125						130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
			140						145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
			155						160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
			170						175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
			185						190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
			200						205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Lys	Pro	Pro	Lys	Ile	
			215						220					225	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
			230						235					240	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
			245						250					255	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
			260						265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
			275						280					285	

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

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Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
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<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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<210> 525

<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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<210> 526

<211> 736

<212> PBT

<213> Homo sapiens

<400> 526

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 20 25 30

Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu
 35 40 45

Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
 50 55 60

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				65					70					75	
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp	
				80					85					90	
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu	
				95					100					105	
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp	
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Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe	
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Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala	
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Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala	
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Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser	
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Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala	
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Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu	
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Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met	
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Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val	
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Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met	
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Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu	
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Gln	Pro	Val	Val	Val	Tyr	Gly	Met	Asp	Tyr	Leu	Gln	Gln	Val	Ser	
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Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr
395 400 405

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213: Artificial Sequence

220:

223: Synthetic oligonucleotide probe

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<400> 580

atgcacagga tttttctggt aa 22

<210> 581

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atgagagaga ttggaatctc aa 22

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caggatag atgtatga 20

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aaatccaac ctgtatcaga tgca 24

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 <400> 591
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 <400> 592
 acaaaaaaaaa gggaacaaaa tacga 25

 <210> 593
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<400> 597
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<400> 598

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<210> 599

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<210> 600

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<223> Synthetic oligonucleotide probe

<400> 600

gactacaagg cgctcagcta 20

<210> 601

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cgggcgggt ctcactctc c 21

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<210> 607
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<400> 607
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<400> 609
cgactccctg agcgagcaga tttcc 25

<210> 610
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<220>
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<400> 610
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<210> 611
<211> 2840
<212> DNA
<213> Homo Sapien

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aacaacaccc aacaactggg gtggggggaa gaaagaaaga aaagaaaccc 150
accacccac caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 200
ctgtggcgcg ccgcctgggt cccgggaaga ctgccagca ccagggggtg 250
ggggagtggg agctgaaagc tctggagag tgagcagccc tagcagggat 300
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 tgggacgttt gtcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612

<211> 352

<212> PRT

<213> Homo Sapien

<400> 612

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Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu
 20 25 30

Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45

Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Trp Leu
 50 55 60

Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75

Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90

Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105

Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Ser Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> G13

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aaataagaaa attctcaagg aggacgagct cttgagttag acccaacaag 150
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
cccaagagga gaaatggggt gaacttctcc cttagctgtgg tggatcatcta 250
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atctgcaggc gcggctccgg gtccctggaga tgtatttcct caatgacact 350
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tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450
aactcacctg ggccgcgctc agccatgagc acttgctgca gcgggtagac 500
aacttcactc agaaccagc gatgttcaga atcaaaggtg aacaaggcgc 550
cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600
gcccgcggg accacctgct gagaaggag ccaagggggc tatgggacga 650
gatggagcaa caggccccctc gggaccccaa ggcccaccgg gagtcaaggg 700
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aaaactcagt gtccgtcagg attgtggca gtagtaaccg aggccgggt 1400
aaacttact acagtgtac tgggggaca atttgagat accagtggca 1450

aaattctgat gccattgtct tctgccgcac gctgggttac tccaaaggaa 1500
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 gcgtctgacc cggaaccct ttcacttctc tgctccogag gtgtcctcgg 1700
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 tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614
 <211> 520
 <212> PRT
 <213> Homo Sapien

<400> 614
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 Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu
 20 25 30
 Ile Asn Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser
 35 40 45
 Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala
 50 55 60
 Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg
 65 70 75
 Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp
 80 85 90
 Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His
 95 100 105
 Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu
 110 115 120
 Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp
 125 130 135
 Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Thr Lys Gly Gln Gln
 140 145 150
 Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro
 155 160 165
 Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys
 170 175 180
 Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

185					190					195				
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln
				200					205					210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
				215					220					225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230					235					240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro
				245					250					255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met
				260					265					270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro
				275					280					285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln
				290					295					300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val
				305					310					315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
				320					325					330
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335					340					345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
				350					355					360
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
				365					370					375
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
				380					385					390
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
				395					400					405
Gly	Gln	Gln	Gln	Val	Lys	Gln	Gln	Lys	Gln	Gln	Arg	Gly	Gln	Asn
				410					415					420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425					430					435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Gln
				440					445					450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455					460					465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615
 <211> 647
 <212> DNA
 <213> Homo Sapien

<400> 615
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 atttaagaag catcctctgc caagaccaa aggaagaag aaaaagggcc 150
 aaaaaccaa atgaaactga tggtaacttg ttccaccatt gggctaactt 200
 tgctgctagg agttcaagcc atgctgcaa atcgcctctc ttgctacaga 250
 aagatactaa aagatcacia ctgtcacaac ctccgggaag gagtagctga 300
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcccc 400
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 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtctcta tatagtgcaa 550
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 647
 <212> PRT
 <213> Homo Sapien

<400> 616
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 20 25 30
 Lys Ile Leu Lys Asp His Asn Tyr His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 aacccgcggt ggtgggttga gggcgccacg tagagcagca gcacagccgc 150
 gggctcccggt aggcgcgctc tgcctgcgcc gagatgtgga atctccttca 200
 cgaaaacgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250
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 caatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450
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<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618

Met	Trp	Asn	Leu	Leu	His	Glu	Thr	Asp	Ser	Ala	Val	Ala	Thr	Ala
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Arg	Arg	Pro	Arg	Trp	Leu	Cys	Ala	Gly	Ala	Leu	Val	Leu	Ala	Gly
				20					25					30

Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
			35						40					45

Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
			50						55					60

Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	His
			65						70					75

Asn	Phe	Thr	Gln	Ile	Pro	His	Leu	Ala	Gly	Thr	Glu	Gln	Asn	Phe
			80						85					90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu
			95						100					105

Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
			110						115					120

Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
			125						130					135

Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Gln	Pro	Pro	Pro	Pro	Gly
			140						145					150

Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
			155						160					165

Pro	Gln	Gly	Met	Pro	Gln	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
			170						175					180

Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
			185						190					195

Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
			200						205					210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Ile	Gly Asn Phe Ser Thr	His Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Glu Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Gln	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Trp	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
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Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Ile	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggtg attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tggaatatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 624

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